

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 19:36:31 ; Search time 2746 Seconds

(without alignments)
10958.595 Million cell updates/sec

Title: US-09-976-605-5

Sequence: 1 aagcttcattgaataagtttaa.....agaagacggaacccctcgag 1034

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rnd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	991.6	95.9	144575	14 YD1293568	AD293568 Yaba-like
2	133.6	12.9	1023	6 ARI45601	ARI45601 Sequence
3	133.6	12.9	1023	6 I58315	I58315 Sequence 53
4	133.6	12.9	3567	14 SWPSPDH	I21931 Swinepox v1
5	133.6	12.9	14176	6 ARI45576	ARI45576 Sequence
6	133.6	12.9	14176	6 ARI45583	ARI45583 Sequence
7	133.6	12.9	14176	6 I58290	I58290 Sequence 1
8	133.6	12.9	14176	6 I58297	I58297 Sequence 14
9	133.6	12.9	14176	14 SWPHLSB	I22013 Swinepox v1
10	133.6	12.9	146454	14 AF410153	AF410153 Swinepox
11	133.6	12.9	146454	14 AF410153	AF410153 Swinepox
12	59.8	5.8	7218	6 I66494	I66494 Sequence 14
13	58.6	5.7	5420	3 AF056936	AF056936 Plasmid
14	57.2	5.5	133501	2 AC116956	AC116956 Dictyoste
15	57	5.5	4102	3 AF270648	AF270648 Plasmid
16	56.8	5.5	216508	10 AL683805	AL683805 Mouse DNA
17	55.4	5.4	1141	6 AX083744	AX083744 Sequence
18	54.8	5.3	914	3 PFRESA	X55124 P. falciparu
19	53.4	5.2	1141	6 AX083744	AX083744 Sequence
20	51.6	5.0	112698	2 AC119418	AC119418 Medicago
21	51.6	5.0	128096	2 AC126019	AC126019 Medicago
22	51.2	5.0	245802	2 AC006279	AC006279 Plasmid
23	51.2	5.0	293431	2 PFMAL13P4	AL049181 Plasmid
24	51.2	4.9	293431	2 PFMAL13P4	AX281184 Sequence
25	50.4	4.9	146383	2 AC116367	AC116367 Oryza sat
26	50.2	4.9	82469	2 AC116330	AC116330 Dictyoste
27	50	4.8	825	3 AF206632	AF206632 Plasmid
28	49.8	4.8	185558	2 AC129389	AC129389 Rattus no
29	49.4	4.8	1686	6 E08995	E08995 DNA encodin
30	49.4	4.8	135599	2 CPU30821	U30821 Cyamophora
31	49.4	4.8	192581	8 PFMAL13P1	AL049180 Plasmid
32	49	4.7	6175	6 AX346209	AX346209 Sequence
33	49	4.7	178098	2 AC040955	AC040955 Mus muscu
34	48.8	4.7	4995	3 PFAMESA	M69183 Plasmid
35	48.8	4.7	60182	2 PFMAL1P6	AL031749 Plasmid
36	48.6	4.7	175159	2 AC097877	AC097877 Rattus no
37	48.6	4.7	182025	9 AL138900	AL138900 Human DNA
38	47.8	4.6	1055	6 AX083745	AX083745 Sequence
39	47.8	4.6	29016	2 AC117266	AC117266 Dictyoste
40	47.6	4.6	1324	3 PFRESA1	X05182 P. falciparu
41	47.6	4.6	4591	6 A00661	A00661 P. falciparu
42	47.6	4.6	245802	2 AC006279	AC006279 Plasmid
43	47.6	4.6	349980	6 AX344559	AX344559 Sequence
44	47.4	4.6	158094	2 AC108623	AC108623 Rattus no
45	47.4	4.6	158255	2 AC112577	AC112577 Rattus no

ALIGNMENTS

RESULT 1	YD1293568/c	144575 bp	DNA	linear	VRL 30-MAY-2001
LOCUS	YD1293568				
DEFINITION	Yaba-like disease virus (YLDV), complete genome.				
ACCESSION	AF293568				
VERSION	AF293568.1	GI:12056159			
KEYWORDS	100L gene; 101L gene; 102R gene; 103L gene; 104L gene; 105L gene; 106L gene; 107L gene; 108L gene; 109L gene; 110L gene; 111L gene; 112L gene; 113L gene; 114R gene; 115R gene; 116R gene; 117L gene; 118L gene; 119L gene; 120L gene; 121L gene; 122R gene; 123R gene; 124R gene; 125R gene; 126R gene; 127R gene; 128L gene; 129R gene; 130L gene; 131R gene; 132R gene; 133L gene; 134R gene; 135R gene; 136R gene; 137R gene; 138R gene; 139R gene; 140R gene; 141R gene; 142R gene; 143R gene; 144R gene; 145R gene; 146R gene; 147R gene; 148R gene; 149R gene;				

14L gene; 150R gene; 151R gene; 15L gene; 16L gene; 17L gene; 18L gene; 19L gene; 1I gene; 20L gene; 21L gene; 22L gene; 23L gene; 24L gene; 25L gene; 26L gene; 27L gene; 28R gene; 29L gene; 2L gene; 3-beta-hydroxysteroid dehydrogenase; 30L gene; 31R gene; 32L gene; 33L gene; 34L gene; 35L gene; 36R gene; 37R gene; 38R gene; 39L gene; 3I gene; 40R gene; 41L gene; 42L gene; 43L gene; 44L gene; 45L gene; 46L gene; 47L gene; 48L gene; 49R gene; 4L gene; 50L gene; 51L gene; 52R gene; 53L gene; 54R gene; 55R gene; 56R gene; 57L gene; 58R gene; 59R gene; 5L gene; 60R gene; 61R gene; 62L gene; 63R gene; 64R gene; 65R gene; 66R gene; 67R gene; 68R gene; 69R gene; 6L gene; 70L gene; 71R gene; 72L gene; 73R gene; 74L gene; 75L gene; 76R gene; 77R gene; 78R gene; 79R gene; 7L gene; 80L gene; 81R gene; 82R gene; 83R gene; 84R gene; 85R gene; 86R gene; 87R gene; 88L gene; 89L gene; 8L gene; 90L gene; 91L gene; 92L gene; 93L gene; 94L gene; 95L gene; 96R gene; 97L gene; 98L gene; 99R gene; 9L gene; CC chemokine receptor; CD46-like protein; CD47-like protein; DNA helicase; DNA polymerase; DNA polymerase processivity factor; DNA topoisomerase I; DNA-binding phosphoprotein; DNA-binding protein; DNA-binding vifron core protein; DN/RNA-binding protein/vifro; dsRNA-binding protein an; dtpase; early transcription factor; eIF2-alpha mimic and anti-interfero; extracellular virus membran; extracellular virus membrane protein; glutaredoxin 2; host range protein; interferon alpha/beta receptor; interleukin-18 binding protein; intermediate gene transcription facto; late gene transcription factor; late gene transcription factor-2; late transcription elongation factor; late transcription factor; mda-7-like or interleukin-10-like; membrane-associated vifron protein; monoglyceride lipase; mRNA capping enzyme large subunit; mRNA capping enzyme small subunit; Mvfr protein; myristylprotein; negative regulator of gene expression; nucleoside triphosphat; poly(A) polymerase catalytic subunit; poly(A) polymerase regulatory subunit; protease; ribonucleotide reductase small subunit; RNA and DNA helicase; RNA polymerase associated transcriptio; RNA polymerase elongation factor; RNA polymerase subunit ipol32; RNA polymerase subunit factor; RNA polymerase subunit ipol3; RNA polymerase subunit ipol4; RNA polymerase subunit ipol5; RNA polymerase subunit ipol9; RNA polymerase subunit ipo22; RNA polymerase subunit ipo30; RNA polymerase subunit ipo35; RNA polymerase subunit ipov; role in virus DNA packaging; secreted OX-2-like protein; secreted protein; serine protease; serine protease inhibitor; serine/threonine protein kinase; soluble MHC-I-like protein; ssDNA-binding phosphoprotein; thymidine kinase; topoisomerase II; transmembrane myristylprotein; uracil DNA glycosylase; vifron core structural protein phosphatase; uracil DNA glycosylase; vifron core structural protein Paa; vifron membrane protein; vifron protein; vifron structural core protein; vifron structural protein; vifron surface protein; virulence factor; virus growth factor.

yaba-like disease virus.
yaba-like disease virus
viruses; dsDNA viruses, no RNA stage; poxviridae; Chordopoxvirinae; Yatapoxvirus. 144575

REFERENCE
AUTHORS
JOURNAL
1 (bases 1 to 144575)
Lee, H. J.
Thesis (2000) Sir William Dunn School of Pathology, University of Oxford, Oxford, UNITED KINGDOM
2 (bases 1 to 144575)
Lee, H. J., Essani, K. and Smith, G. L.
The genome sequence of Yaba-like disease virus, a yatapoxvirus
Virology 281 (2), 170-192 (2001)
MEDLINE
21176366
PUBMED
11277691
REFERENCE
AUTHORS
JOURNAL
3 (bases 1 to 144575)
Lee, H. J.
Direct Submission
Submitted (13-JUL-2000) Lee H. J., Sir William Dunn School of Pathology, University of Oxford, Oxford, UNITED KINGDOM

```
FEATURES
  source
    location/Qualifiers
      1..144575
        /organism="Yaba-like disease virus"
        /viflon
        /db_xref="taxon:132475"
        complement(755..1756)
  gene
```

```

/gene="IL"
/complement(755. .1756)
/gene="IL"
/function="Unknown"
/citation[2]
/codon_start=1
/product="IL protein"
/protein_id="CAC21239.1"
/db_xref="GI:12056160"
/db_xref="SPTREMBL:Q9DQJ2"
/translation="MEVITDGLRLKSPDDEFGIKKEELKFLMNSMEDSDILRHROTL
PCRLILLESSEETKQYFAVAKVIRVLASSIITLNYNYVEHLIYKCRGQVFNRSRIS
EDHRGRFTTIVLHLSSPKNGSKTDVCGKYIVISPRADFLIKESQSLNVSQGEKE
IVLVYRFTLRKADYITFLARFVWKEKTFVDMCTESLSEFTVLSVWESGKDMANLELAAV
EDLSGSSSEEDYKFLRELVYVSSNLTKRDYVYLSTCDDETFQVYSLNRCYFSI
TIDWVSSSEEDYKFLRELVYVSSNLTKRDYVYLSTCDDETFQVYSLNRCYFSI"
/complement(1869. .2885)
/gene="2L"
/complement(1869. .2885)
/gene="2L"
/complement(1869. .2885)
/gene="2L"
/complement(1869. .2885)

```

```

/funcion="putative soluble MHC-I-like protein"
/note="related to swinepox virus C1L and chicken MHC-I"
/citation=[2]
/codon_start=1
/product="2L protein"
/protein_id="CAC21240.1"
/db_xref="GI:12056161"
/db_xref="SPREMBL:Q9D8M0"
/translation="MDKLLFSTIVAVNCNLTLYNTVTLLKDGGLYDGVFYDHNDL
LVTRISINHTHRTGGLVNFRAADFNISRSPPHNGDYNFNWYSILAKETLEINRKNDS
KTSLSLISNHTHRTGGLVNFRAADFNISRSPPHNGDYNFNWYSILAKETLEINRKNDS
NTMLKDYKAIAGSEFYMGCSLIILDQYCMAGKIKPIKPTPTVTVGNELDENMMLKE
TVNSFYPPDYITKTISEHFKCEYRYVNGRIYPRMGKSNYEGEGEPMMNLIKQKQD
NYSFLYDLVATTSYKMSQPCVCFVFDHTLEAOVYTCSECGNELIIDLILYKRTDEGCE
DEED"
complement(2838. .2885)
/gene="2L"
/citation=[2]
complement(2932. .3600)
/gene="3L"
complement(2932. .3600)

```

s1q_peptide
 complement(2838. .2885)
 /gene="2L"
 /citation=[2]
 complement(2932. .3600)
 /gene="3L"
 complement(2932. .3600)
 /gene="3L"
 /function="Unknown"
 /note="related to swinepox virus C5L and vaccinia virus strain Copenhagen K7R"
 /citation=[2]
 /codon_start=1
 /product="3L protein"
 /protein_id="C6C2141.1"
 /db_xref="GI:12056162"
 /db_xref="SPTREMBL:O9DHV9"
 /translation="MEIRKIMERYIKLMSKEAFOCSIFWVNADEFYDQSPNINE
 LKIRIEPGCGNRLIYLDIISYTRKVCMLKDENNLLITSYLNKKLNEFKMKRV
 KNSIDILIIYFPRYKKNNNNIYSCGVRPELMKDEIAKROYEKLHKDINNKKNN
 LRINLYEFNDPILNTCKVSIQFVSIIDVPLPIYNPDPEFNQVSIRIKMLKEEL
 STIN"
 complement(3630. .4346)
 /gene="4L"
 complement(3630. .4346)
 /gene="4L"
 /function="Unknown"
 /note="related to swinepox virus C5L and vaccinia virus strain Copenhagen NZL"
 /citation=[2]
 /codon_start=1
 /product="4L protein"
 /protein_id="CAC21242.1"
 /db_xref="GI:12056163"
 /db_xref="SPTREMBL:O9DHV8"
 /translation="MDYKSLITRYKVCIRKSNKNVEEKKNFSESDIDPTEDE
 VGIFEEELQCTFYTLIOLIKSIIMNQEVLTEIMSLKDONYFENIYTYLIPGHLV
 SMSVSNINIMKEEYEFSPONNNNNIINHGKLFRTIMSYDELAINHGOLYINAIIV
 INSPDVSFSIYKRRKIDITVNIIDIFIKIIGFISILSHVDVYDNPISYIF

gene
DISFTHRQMFKNYLTSLYP"
complement(4386..4856)
/gene="5L"
complement(4386..4856)
/gene="5L"
/function="unknown"
/note="related to swinepox virus CTL"
/citation=[2]
/product="5L protein"
/protein_id="CAC21243.1"
/db_xref="GI:12056164"
/db_xref="SPTREMBL:Q9DHV7"
/translation="MSDLCICNDVCDERNNEFCGNEEKVHIKCMOLINYSKKE
CNCKTKYNIKRYVSFKKNNCFNDKKTFFKIFLFAVFIPLTTLTSDNANLV
TGINDICSIIEIVTYVLTISCEFSYVVAIVDFLEKKNSEFLTEIY"
complement(4920..5369)
/gene="6L"
complement(4920..5369)
/gene="6L"
/function="unknown"
/note="related to vaccinia virus strain Copenhagen B15R"
/citation=[2]
/product="6L protein"
/protein_id="CAC21244.1"
/db_xref="GI:12056165"
/db_xref="SPTREMBL:Q9DHV6"
/translation="MECPGYCLVCLNRRDDIROIIVDYIYMSYSRSPAGKYP
OVLKMFRRSEIIVGENFRHIVKNEKTLGIEDTVOAVKCFIENALRESYMSWDLCA
SLAEYWGSDLEPNDLSLOAKIMTILSDDDYSFIDCLARKRKIK"
complement(5433..6488)
/gene="7L"
complement(5433..6488)
/gene="7L"
/function="putative CC chemokine receptor"
/note="related to Macaca mulatta chemokine receptor and
human CC chemokine receptor type 8"
/citation=[2]
/product="7L protein"

Query Match 95.9%; Score 991.6; DB 14; Length 144575;
Best Local Similarity 98.1%; Pred. No. 2.3e-179;
Matches 1003; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Db 7 CATGATATAGTTAATATATTATTTAGCACATTTGTACAGTTTGTATGCAATTAATTAA 66
|||||
2886 CATGATATAGTTAATATATTATTTAGCACATTTGTACAGTTTGTATGCAATTAATTAA 2827

Qy 67 ATATATATATCTGTAGTAAAGATATGGTTATAGATGAGTATTTTACGATCA 126
|||||
2826 ATATATATATCTGTAGTAAAGATGATGGTTATAGATGAGTATTTTACGATCA 2767

Db 127 TTACACGATCAGTTAGTACGAAATATCATATATACGAAACTAGACAGGAAACGT 186
|||||
2766 TTACACGATCAGTTAGTACGAAATATCATATATACGAAACTAGACAGGAAACGT 2707

Qy 187 AAATTTAGGCTATGGTTATTTCTAGAGTCCCAACAGCCAGGTAAAGATTA 246
|||||
2706 AAATTTAGGCTATGGTTATTTCTAGAGTCCCAACAGCCAGGTAAAGATTA 2647

Db 247 CAACCTTAACTTTGGTATCTTTAATGAAGAACTTTAGAGAAATTAATTAAGCA 306
|||||
2646 TAACTTTAACTTTGGTATCTTTAATGAAGAACTTTAGAGAAATTAATTAAGCA 2587

Qy 307 TAGACAAAAAATCTCGCTTTCATTAATCACTGGGTGTATGAAGAGATTAATAT 366
|||||
2586 TAGACAAAAAATCTCGCTTTCATTAATCACTGGGTGTATGAAGAGATTAATAT 2527

Db 367 TGTAGTATATGGTATAGAAAGCGCAAGCGGTGGCCAGATACCATACAGGAA 426
|||||
2526 TGTAGTATATGGTATAGAAAGCGCAAGCGGTGGCCAGATACCATACAGGAA 2467

Qy 427 TAAAGGTTTACGAAAAATGACACATTAAGGTTTCCCAAGGTTGAATGTAACGTAA 486
|||||
2466 TAAAGGTTTACGAAAAATGACACATTAAGGTTTCCCAAGGTTGAATGTAACGTAA 2407

Db 487 AAACACCTTTGGAAAAATATGTTAAACTTATCTAGCCGGTTTGAATACATGGATGTC 546
|||||
2406 AAACACCTTTGGAAAAATATGTTAAACTTATCTAGCCGGTTTGAATATATGATGTC 2347

Qy 547 ATTAGCTATTTTATGATTATACCAAAAAATGGCTAAAGGTGAATATCCAAAAATCAACAC 606
|||||
2346 ATTAGCTATTTTATGATTATACCAAAAAATGGCTAAAGGTGAATATCCAAAAATCAACAC 2287

Db 607 TACAGTAAAACTAACGGGTATAGTATGAAGATGTGAACATGCTTGAATGAGTGT 666
|||||
2286 TACAGTAAAACTAACGGGTATAGTATGAAGATGTGAACATGCTTGAATGAGTGT 2227

Qy 667 AAATTCATTTTACCCTGACGTATTTACTAAGTGTAGAAAGCAATTTTAAAG 726
|||||
2226 AAATTCATTTTACCCTGACGTATTTACTAAGTGTAGAAAGCAATTTTAAAG 2167

Db 727 TGAATATTAATATGTTAAGGAAAGATCTATCCAGATGGGGAGAAAAATCCAGTTATGA 786
|||||
2166 TGAATATTAATATGTTAAGGAAAGATCTATCCAGATGGGGAGAAAAATCCAGTTATGA 2107

Qy 787 GCCAGAGAGCCAGGTTTCCATGCAATTTTAAAAAGATTAAGTGAACATATATG 846
|||||
2106 GCCAGAGAGCCAGGTTTCCATGCAATTTTAAAAAGATTAAGTGAACATATATG 2047

Db 847 TTTAAGATTTAGTACGTACAAACATCAAAAAATGAGTGTGAACAGATATGTGTTT 906
|||||
2046 TTTAAGATTTAGTACGTACAAACATCAAAAAATGAGTGTGAACAGATATGTGTTT 1987

Qy 907 CCATGACCTTTTGAAGCCAGTTTATCTGTTCTGAAGATGCAATGAGAGCTATA 966
|||||
1986 CCATGACCTTTTGAAGCCAGTTTATCTGTTCTGAAGATGCAATGAGAGCTATA 1927

Db 967 CGACCACTATATAGAAAAAGAGAGAGAGAGTGAAGATGAAGAGCAAGCGAAA 1026
|||||
1926 CGATCACCTATATAGAAAAAGAGAGAGAGAGTGAAGATGAAGAGCAAGCGAAA 1867

Qy 1027 CC 1028
||
1866 CC 1865

Db 1027 CC 1028
||
1866 CC 1865

RESULT 2
ARI45601 1023 bp DNA linear PAT 08-AUG-2001

LOCUS ARI45601
DEFINITION Sequence 53 from patent US 6217882.
ACCESSION ARI45601
VERSION ARI45601.1 GI:15108790
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
Unclassified.
1 (bases 1 to 1023)
AUTHORS Moyer, R.W., Vinuela, E. and Gibbs, E.P.J.
TITLE Use of recombinant swine poxvirus as a live vaccine vector
JOURNAL Patent: US 6217882-A 53 17-APR-2001;
FEATURES
source location/Qualifiers
1..1023
/organism="unknown"
BASE COUNT 359 a 158 c 199 g 307 t
ORIGIN

Query Match 12.9%; Score 133.6; DB 6; Length 1023;
Best Local Similarity 49.0%; Pred. No. 9e-16;
Matches 451; Conservative 0; Mismatches 454; Indels 15; Gaps 3;

Qy 27 TTACACAAATTTGACAGTTTGTAACTGATTAATTAATTAATTAATTAATTAATTA 86
|||||
35 TTACACAAATTTGACAGTTTGTAACTGATTAATTAATTAATTAATTAATTAATTA 94

QY 861 TACGTACACATCAAAAATGAGTCACTAGTGTGTTTCCATGACACTTTAG 920
 DB 3405 TTATGTACCAACTATCATCTTAATGATATGACATGTTGATTCATAGTACCTTAG 3464
 QY 921 AAGCGCAAGTTTACTTGT 940
 DB 3465 AACCAAGCATATATGATGT 3484

RESULT 5
 ARI45576/c 14176 bp DNA linear PAT 08-AUG-2001
 LOCUS Sequence 1 from patent US 6217882.
 ARI45576
 VERSION ARI45576.1 GI:15108765
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 14176)
 AUTHORS Moyer, R.W., Vinuela, E. and Gibbs, E.P.J.
 TITLE Use of recombinant swine poxvirus as a live vaccine vector
 JOURNAL Patent: US 6217882-A 1 17-Apr-2001;
 FEATURES Location/Qualifiers
 source 1..14176
 BASE COUNT 4820 a 2231 c 1639 g 5486 t
 ORIGIN

Query Match 12.9%; Score 133.6; DB 6; Length 14176;
 Best Local Similarity 49.0%; Pred. No. 5.7e-16;
 Matches 451; Conservative 0; Mismatches 454; Indels 15; Gaps 3;

QY 27 TTACGACATTTGACAGTTTGTATCTGATTAATTAATTAATTAATCTTACT 86
 DB 994 TTACGACATTTGATGATCTTCCGATCTTATGATTAATTAATTAATTAATCAAG 935
 QY 87 TAAAGATATATGGTTATGATGATGATTTTATGATTAATTAATTAATTAATTAAT 146
 DB 934 ATGATATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 875
 QY 147 CGAAATATCATATATACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 206
 DB 874 GTTAAATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 815
 QY 207 TTAATATTTCTAGAGTCCCGACAGCCAGTATGATTAATTAATTAATTAATTAAT 266
 DB 814 TTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 755
 QY 267 CTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 323
 DB 754 ATAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 695
 QY 324 ---CGCTTTCATTAATCTAGTGTGATGATGATGATGATGATGATGATGATGATGAT 380
 DB 694 AGACTATGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 635
 QY 381 ATGTAGAAAGCGCAAGCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 440
 DB 634 ATGTATCTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 575
 QY 441 AATGACATTAAGGTTTCCCAAGGTTGATGATGATGATGATGATGATGATGATGATGAT 500
 DB 574 AAGTTGATCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 515
 QY 501 AAGATTAATAAATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 560
 DB 514 AACGTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 455
 QY 561 ATTACCAAAAATGCTTAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 620
 DB 454 ATTATATTAATAATTTCTAAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 395

QY 621 CGGTATAGAGTTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 680
 DB 394 CAGGATTTGAAAGAGAGAG---TAATCTATCTATGATGATGATGATGATGATGATGATGAT 338
 QY 681 CTCCTGACGTAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 740
 DB 337 CCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 278
 QY 741 TTAAGGAAAGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 800
 DB 277 ATCCG-----TACGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 224
 QY 801 GTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 860
 DB 223 GATATCCGACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 164
 QY 861 TACGTACCAATCAAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 920
 DB 163 TTATGTACCAACTATCATGATCTAATGATGATGATGATGATGATGATGATGATGATGAT 104
 QY 921 AAGCGCAAGTTTACTTGT 940
 DB 103 AACCAAGCATATATGATGT 84

RESULT 6
 ARI45583 14176 bp DNA linear PAT 08-AUG-2001
 LOCUS Sequence 14 from patent US 6217882.
 ARI45583
 VERSION ARI45583.1 GI:15108772
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 14176)
 AUTHORS Moyer, R.W., Vinuela, E. and Gibbs, E.P.J.
 TITLE Use of recombinant swine poxvirus as a live vaccine vector
 JOURNAL Patent: US 6217882-A 14 17-Apr-2001;
 FEATURES Location/Qualifiers
 source 1..14176
 BASE COUNT 5486 a 1639 c 2231 g 4820 t
 ORIGIN

Query Match 12.9%; Score 133.6; DB 6; Length 14176;
 Best Local Similarity 49.0%; Pred. No. 5.7e-16;
 Matches 451; Conservative 0; Mismatches 454; Indels 15; Gaps 3;

QY 27 TTACGACATTTGACAGTTTGTATCTGATTAATTAATTAATTAATTAATCTTACT 86
 DB 13183 TTACGACATTTGATGATCTTCCGATCTTATGATTAATTAATTAATTAATTAATCAAG 13242
 QY 87 TAAAGATATATGGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 146
 DB 13243 ATGATATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 13302
 QY 147 CGAAATATCATATATACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 206
 DB 13303 GTTAAATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 13362
 QY 207 TTAATATTTCTAGAGTCCCGACAGCCAGTATGATTAATTAATTAATTAATTAATTAAT 266
 DB 13363 TTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 13422
 QY 267 CTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 323
 DB 13423 ATAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 13482
 QY 324 ---CGCTTTCATTAATCTAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 380
 DB 13483 AGACTATGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 13542

[illegible]

RESULT 8				
158297				
LOCUS	158297	14176 bp	DNA	linear
DEFINITION	Sequence 14 from patent US 5651972.			
ACCESSION	158297			
VERSION	158297.1			
KEYWORDS	.GI:2477535			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
1 (bases 1 to 14176)				
Authors	Moyer, R.W., Vinuela, E. and Gibbs, E. P. J.			
Journal	Use of recombinant swine poxvirus as a live vaccine vector			
Patent:	US 5651972-A 14 28-JUL-1997;			
Location/Qualifiers				

Matches 218; Conservative 0; Mismatches 244; Indels 3; Gaps 1;

QY 559 AGATTACCAAAAATGCTAAAGTGAATACCAAAAGATACCAACCTACAGTGAAGT 618
 Db 4090 AGTTAAAAAGAGTAAAAAGAAATATTAATAAGAAACCAAGATATGTGATAGT 4149
 QY 619 AAGGGTAAAGATTAAGATGTACATGACTCTTGAATGCAAGTGAATTCATTTTA 678
 Db 4150 ACAAAGAAATTAATGACCAAGATGTTAAACGAAAAAGATCCGAAAGCAAGATTAATGAT 4209
 QY 679 CCTCTACAGTAAATCTAAAGTGAATAGCAAGCAATTTAAAGGTCAATATTAATA 738
 Db 4210 AGAAAAAGAAATATATATAGAGAGTAAAGAAAGATTAATAAGAGTAAACAAAGA 4269
 QY 739 TGTTAACGGAAGATCTATTCAGAAATGGGGAGAAATCCGATTTAGCCAGAGAGCC 798
 Db 4270 AGTTAACAAAAAGATTAACAGAAATAGAAAAATGAAGAAGAAATGCTGATAGACA 4329
 QY 799 AGTTTTCATGGAATTTTAAAAAGATTAAGTGC---AAACACATATATGTTTAACAGA 855
 Db 4330 AGAAATAGTAAAGCAAGAGTAAACGAAAAAGATACCAAAACACGATTAAGATAGG 4389
 QY 856 TTTTAGTACGTACACATCAAAAATGAGTCAACTAGTATGTGTTTCCATGACAC 915
 Db 4390 AAAAAAGTCAAAAACCAATAGATGATTTGTAATAAGAAAGAAAGATACAGAAAGATC 4449
 QY 916 TTTAGAGCGCAAGTTTACTTGTCTGAGAGTCAATGAGAGCTATACGACACCT 975
 Db 4450 TGAAGAGAGTCTGAAGAGAGTCTGAAGAGAACTGTAAGAGAGTCTGAAGAGAAATC 4509
 QY 976 ATATAGAAAAACAGAAAGAGAGAGTGAAGAGATGAGAGAGAGA 1020
 Db 4510 TGAAGAGAGTCTGAAGAGAAATCTGAAGAGAGTCTGAAGAGAGA 4554

RESULT 14

AC116956 133501 bp DNA linear HTG 04-APR-2002
 LOCUS AC116956
 DEFINITION Dictyostelium discoideum chromosome 2 map 1512060-1645559 strain AX4, *** SEQUENCING IN PROGRESS ***, in ordered pieces.

ACCESSION AC116956
 VERSION AC116956.1 GI:19919988
 KEYWORDS HTG; HTGS_PHASE2.
 SOURCE Dictyostelium discoideum.
 ORGANISM Dictyostelium discoideum.
 REFERENCE 1 (bases 1 to 133501)
 Eukaryota; Mycetozoa; Dictyostelidae; Dictyostelium.

AUTHORS Gloeckner, G., Eichinger, L., Szafranski, K., Pachebat, J., Dear, P.,
 Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K.,
 Tunngal, B., Cox, E., Quail, M. A., Platzer, M., Rosenblatt, A. and
 Noegel, A. A.

TITLE Sequence and Analysis of Chromosome 2 of Dictyostelium
 JOURNAL Unpublished
 REMARK The Dictyostelium Genome Sequencing Consortium
 AUTHORS 2 (bases 1 to 133501).
 JOURNAL Baumgart, C.

COMMENT Direct Submission
 Submitted (04-APR-2002) Genome Analysis, Institute of Molecular
 Biotechnology, Beutenbergstr. 11, Jena 07745, Germany
 is available from IMB Jena, Department of Genome Analysis
 (http://genome.imb-jena.de/dictyostelium/)
 and the University Cologne, Institute for Biochemistry I
 (http://www.uni-koeln.de/dictyostelium/project.shtml)

FEATURES
 source
 1. 133501
 Location/Qualifiers
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.

/organism="Dictyostelium discoideum"

Query Match
 Best Local Similarity 5.5%; Score 57.2; DB 2; Length 133501;
 Matches 379; Conservative 0; Mismatches 478; Indels 5; Gaps 3;

QY 17 TTAATATATTTACACAAATTTGAGCTTTGTAACGTACTTAAATATATATAT 76
 Db 97394 TTTGTTTTTTTACAAATTTGGGAAAAAGATTTGCAATTAAGATCAAAACGTTAAAT 97335
 QY 77 ACTGTTACGTTAAAGATTAATGAGTATGATGATGATGATGATGATGATGATGAT 136
 Db 97334 CCTTAAAT 97275
 QY 137 CAGTTAGTAAAGAAAT 196
 Db 97274 TA-TTAT 97216
 QY 197 GCTGATGCTTTAT 256
 Db 97215 ACTGAT 97156
 QY 257 TTTTGGTATCTTATATGAAAGAACTTTGAGAAATTAATTAATAAAGCATGACAA 316
 Db 97155 TTTTAT 97096
 QY 317 ACTACTGCTTCAATTAATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 376
 Db 97095 AATAAATAATTTACTAT 97036
 QY 377 GGGTATGTAAGAAAGCGCAAGGACCGTTGGCCAGATACATACAGATTAAGATTA 436
 Db 97035 GTGGTAAATTAATAAATCTTTTGGTTTGGGTGGTGTATTTTAAAAAATAAT 96976
 QY 437 ACGAAATGACACATTAAGGTTTCCCAAGCTGGAATGCTTAACGTAAAAACCTCT 496
 Db 96975 AAAAAAATTAACAAATTAATAAAGAGAAATGGAAAAAATAAATAAATAAATAA 96916
 QY 497 TGAAGAGATGAATAAATCTATAGCGGTTTGAATACATGAGATGTTCAATTAGCT 556
 Db 96915 AAAAAAATAAATAAATTAAGTCAATAGCGTCAATTTTGGATATATATATATAT 96856
 QY 557 TTGATTACCAAAAAATGCTAAAGTGAATATACAAAGATACAAACCTACAGTGA 616
 Db 96855 AATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 96798
 QY 617 GTACGCTTAATGATTAAGATGATGATGATGATGATGATGATGATGATGATGAT 676
 Db 96797 TGAAGAGATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 96738
 QY 677 TACCCCTGACGTATTTCTAATGATGATGATGATGATGATGATGATGATGATGAT 736
 Db 96737 TACCTTATTTG-GTAAATTAATAAATAAATAAATAAATAAATAAATAAATAA 96680
 QY 737 TATGTTACGGAAGATTAATCAAGATGAGAGGAGAAATCCGATTTATGAGCCAGG 796
 Db 96679 TAATAAATAATATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 96620
 QY 797 CCAGGTTTCCATGGAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAA 856
 Db 96619 TCTGATTTGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 96560
 QY 857 TTAGTACGTACAACTCAAAAA 878
 Db 96559 TTAATAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 96538

RESULT 15

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 19:09:36 ; Search time 290 Seconds
(without alignments)
8029.539 Million cell updates/sec

Title: US-09-976-605-5

Perfect score: 1034
Sequence: 1 aagcttcacgaataagtttaa.....agaagacggaacccctcgag 1034

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1034	100.0	1034	AAD37916	Tanapox virus (TPV)
2	986.6	95.4	1017	AAD37917	Yaba-like disease
3	571.6	55.3	1183	AAD37946	Yaba monkey tumor
4	133.6	12.9	1023	AAD37918	Swinepox virus (CI)
5	133.6	12.9	14176	AAR4564	Swinepox virus (CI)
6	133.6	12.9	14176	AAR4948	Nucleotide sequence
7	133.6	12.9	14176	AAR4949	Reverse complement
8	98	9.5	183	AAD37915	Yaba monkey tumor
9	51	4.9	6306	ABL49349	Human polynucleotl

10	49.4	4.8	1686	16	AA087587
11	49	4.7	6175	24	ABL33307
12	47.6	4.6	4590	7	AA060472
13	47.2	4.6	3399	17	AA05868
14	47	4.5	6012	24	ABL70327
15	47	4.5	6012	24	AA061274
16	47	4.5	6012	24	ABK31370
17	45.8	4.4	4590	22	AA026065
18	45.2	4.4	3579	21	AA070099
19	44.8	4.3	423	23	AA090685
20	44.8	4.3	1866	21	AA096533
21	44.8	4.3	1998	21	AA070212
22	44.8	4.3	15548	24	ABL34155
23	44.6	4.3	7195	22	AA045325
24	44.6	4.3	7195	22	ABK28166
25	44.4	4.3	5454	21	AA070189
26	43.8	4.2	18512	24	ABL32976
27	43.6	4.2	8622	24	ABL34142
28	43.4	4.2	5454	21	AA070236
29	43.2	4.2	801	24	AB069391
30	43.2	4.2	810	24	AB067695
31	43.2	4.2	1269	20	AA096678
32	43.2	4.2	7536	24	ABL33464
33	43.2	4.2	15954	24	ABL70468
34	43.2	4.2	15954	24	ABK31495
35	43.2	4.2	1163020	24	AB067197
36	43.2	4.2	3011208	24	AB069245
37	42.6	4.1	143899	24	AA183836
38	42	4.1	1956	18	AA067161
39	42	4.1	7458	21	AA070106
40	41.8	4.0	1887	20	AA099539
41	41.8	4.0	3078	20	AA099554
42	41.8	4.0	3288	23	ABL19706
43	41.8	4.0	3808	23	ABL19707
44	41.8	4.0	4849	23	ABL14832
45	41.8	4.0	6071	24	ABL32324

ALIGNMENTS

RESULT 1	
AD37916	
ID	AAD37916 standard; DNA; 1034 BP.
XX	
XX	AAD37916;
AC	
XX	
DT	10-SEP-2002 (first entry)
XX	
DE	Tanapox virus (TPV) gp38 DNA.
XX	
KW	Immunomodulatory disorder; gp38; cancer; inflammation; allergic reaction;
KW	tumour; transplant rejection; restenosis; autoimmune complication; AIDS;
KW	acquired immune deficiency syndrome; antibody complex mediated disease;
KW	pericarditis; Behcet's syndrome; acute respiratory distress syndrome; AIDS;
KW	ischemic heart disease; atherosclerosis; leukaemia; Addison's disease;
KW	type I insulin-dependent diabetes mellitus; atherosclerosis; cytostatic;
KW	gene therapy; antibacterial; cardiant; vasotrophic; virucide; TPV;
KW	Tanapox virus; gene; ds.
XX	
OS	Tanapox virus.
XX	
Key	Location/Qualifiers
FT	8..1021
FT	/*tag= a
FT	/product= "TPV gp38 protein"
FT	/transl_except= (pos:209..211, aa:Lys)
FT	/note= "CDS does not include stop codon"
FT	/partial
XX	
PN	W0200231115-A2.
XX	
PD	18-APR-2002.

DNA encoding Leuco
Human immune syste
Sequence encoding
Chicken leucocytoz
Chemically treated
Human gene regulat
Signal transductio
Yeast AOD9604-asso
Plasmodium falcipa
DNA encoding novel
Nucleic acid seque
Plasmodium falcipa
Human immune syste
Chemically pretra
DNA transcription
Plasmodium falcipa
Human immune syste
Human immune syste
Plasmodium falcipa
Listeria innocua D
Nucleic acid seque
Human immune syste
Chemically treated
Signal transductio
Listeria innocua C
Listeria innocua D
Genomic sequence e
Plasmodium falcipa
Plasmodium falcipa
Nucleic acid seque
Nucleic acid seque
Drosophila melanog
Drosophila melanog
Drosophila melanog
Human immune syste

601 A C A G T G A A G T A C C C C T A T C T C C T T C C T C C C T C C C T C C C T

PT New Yatapoxvirus

treating immunomodulatory disorders, e.g. cancer, transplant rejection
asthma, ischemic heart disease, atherosclerosis, or systemic lupus

PT erythematosis
 XX
 PS Claim 18: Page 71; 75pp; English.
 XX
 CC The present invention relates to novel Yatapoxvirus immunomodulatory
 CC peptides, gp38 and nucleic acid molecules encoding such proteins.
 CC Sequences of the invention are useful for treating immunomodulatory
 CC disorders such as cancers, tumours, inflammation, allergic reactions,
 CC transplant rejection, reestenosis, antibody complex mediated diseases,
 CC autoimmune complications of AIDS (acquired immune deficiency syndrome),
 CC psoriasis, Behcet's syndrome, acute respiratory distress syndrome (ARDS),
 CC ischemic heart disease, type I insulin-dependent diabetes mellitus,
 CC Addison's disease, atherosclerosis or leukemia. They are also used in
 CC gene therapy. The present sequence is Yaba monkey tumor virus (YMTV)
 CC gp38 DNA.
 CC
 SQ Sequence 1183 BP: 378 A; 179 C; 285 G; 341 T; 0 other;
 Query Match 55.3%; Score 571.6; DB 24; Length 1183;
 Best Local Similarity 74.5%; Pred. No. 4,7e-121;
 Matches 763; Conservative 0; Mismatches 249; Indels 12; Gaps 3;
 Oy 8 ATGATATAGTATATATTA---TTTACGCAATTTGTAGCAGTTGTATGATCACTTAA 64
 Db 1 ATGATATAGTATATATTTATCGTTGTGTTGTGCGCACTTGCAATGTATTAACCTTA 60
 Oy 65 AATATATATTTACTGTAGCTTAAAGATATAGGCTTATACATGAGTATTTTACGAT 124
 Db 61 AGATATATATTTATACCGTTACGTTAAG---AATGATATATACAGCGGGTATTTTGTAT 117
 Oy 125 CATTTACAGATCATGATTAAGTATACGAAATATCATATACACGAACTAGACAGGAAC 184
 Db 118 TATTTACAGATCATGATTAAGTATACAGATATCATATACATGAACTAGACAGGAAC 177
 Oy 185 GTAATTTTACGGCTGATGTTTATATTTCTTGAGAGTCCCAACGCGAGGTAAAGAT 244
 Db 178 GTAATTTTACGGCTGATGTTTATATTTCTTGAGAGTCCCAACGCGAGGTAAAGAT 237
 Oy 245 TACACTTTTACTTTGGTATCTTATATGAAAGAACTTTAGA-----AGAAATTAAT 298
 Db 238 TACACTTTTACTTTGGTATCTTATATGAAAGAACTTTAGA-----AGAAATTAAT 297
 Oy 299 AAAAAAGATGACAAAAAATCTACTTCGTTTCAATTAATCACTGGGTGTATGAACAGGA 358
 Db 298 AAAAAAGATGACAAAAAATCTACTTCGTTTCAATTAATTTGGGGTGTATGAACAGGA 357
 Oy 359 TATATTTTGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 418
 Db 358 TCTCTTTTGGGAGTACGATACGATACGATACGATACGATACGATACGATACGATACG 417
 Oy 419 ACAGAGATTAAGGTTTACGAAATGACATTAAGGTTTCCAAAGTTGGAATGTTA 478
 Db 418 ACAGAGATTAAGGTTTAAATGACATTAAGGTTTCCAAAGTTGGAATGTTA 477
 Oy 479 ACTGTAAAAAATCTTTGGAAGATGATTAAGGTTTCTAGAGGTTTGAATACATG 538
 Db 478 ACCGTTCATGTCCTAGTGTGCAACAGTTAAAAATGCTGGGGGTTTGTATACGCT 537
 Oy 539 GGATGTCATGATCTTTTATAGTATACCAAAAAATGCTTAAAGGTAATACCAAAAGAT 598
 Db 538 GGATGTCATGATCTTTTATAGTATACCAAAAAATGCTTAAAGGTAATACCAAAAGAT 597
 Oy 599 ACACACCTTACAGTGAAGTAAACGGGTAATGAGTAAAGATGTAACATGATCTTTGAA 658
 Db 598 GTAAATGCAACTGTACGTAACGGGTAGAGTAACGTAAGGTTGTAACACACGCTTAAG 657
 Oy 659 TGCAGTGTAAATCATTTTACCTCTGACGTAATTAAGTGTGTAAGGAAGCAAT 718
 Db 658 TGTACGTAATTAATCTTTTACCTCTGACGTAATTAAGTGTGTAAGGAAGCAAT 717
 Oy 719 TTTAAAGGTATATATATGTTAAAGGATATCTATCCAGAAATGGGGGAGAAATCC 778
 Db 718 TTTAAAGGTATATATATGTTAAAGGATATCTATCCAGAAATGGGGGAGCAATCA 777

Oy 779 GATTATAGCAGAGAGCCAGGTTTTCATGATATTAAGATTAAGATCAAAAC 838
 Db 778 GATTATAGCAGCAGAGAGCCAGGTTTTCATGATATTAAGATTAAGATCAAAAC 837
 Oy 839 ACATATAGTTTAAACAGATTTAGTACATACATCAAAATGATGATGATGATGATGAT 898
 Db 838 ACATATAGTTTAAACAGATTTAGTACATACATCAAAATGATGATGATGATGATGAT 897
 Oy 899 GTTGTTCATGACCTTTAGAGGCAAGTTTATCTGTTGTAAGGATGCAATGGA 958
 Db 898 GTTGTTCATGACCTTTAGAGGCAAGTTTATCTGTTGTAAGGATGCAATGGA 957
 Oy 959 GAGTATACGACCACTTATATAGAAACAGAAAGGAAAGGTAAGGATGAGAA 1018
 Db 958 AATATATAGATACCTATATAGAAATGCAAGAGAGAGGTTGTGAGAGAGCA 1017
 Oy 1019 GACG 1022
 Db 1018 GAAG 1021

RESULT 4
 AAD37918
 ID AAD37918 standard; DNA; 1023 BP.

AAD37918;
 10-SEP-2002 (first entry)
 Swinepox virus (CIL) p38 DNA.

Immunomodulatory disorder; gp38; cancer; inflammation; allergic reaction;
 tumor; transplant rejection; reestenosis; autoimmune complication; AIDS;
 acquired immune deficiency syndrome; acute respiratory distress syndrome; ARDS;
 psoriasis; Behcet's syndrome; acute respiratory distress syndrome; ARDS;
 ischemic heart disease; atherosclerosis; leukemia; Addison's disease;
 type I insulin-dependent diabetes mellitus; atherosclerosis; cytostatic;
 gene therapy; antibacterial; cardiant; vasotropic; virocid; CIL;
 swinepox virus; gene; ds.

Swinepox virus.

Key Location/Qualifiers
 CDS 1..1023
 FT /*tag= a
 FT /product= "CIL gp38 protein"

WO200231115-A2.

18-APR-2002.

11-OCT-2001; 2001WO-US32136.

11-OCT-2000; 2000US-239354P.

(VIRO-) VIRION THERAPEUTICS INC.

McFadden G, Essani K;

WPI; 2002-452345/48.

P-PDB; AAE23671.

New Yatapoxvirus immunomodulatory polypeptide, gp38, useful for
 treating immunomodulatory disorders, e.g. cancer, transplant rejection,
 asthma, ischemic heart disease, atherosclerosis, or systemic lupus
 erythematosis
 Disclosure; Fig 8; 75pp; English.

The present invention relates to novel Yatapoxvirus immunomodulatory
 peptides, gp38 and nucleic acid molecules encoding such proteins.
 Sequences of the invention are useful for treating immunomodulatory

AC	AAF84948;
XX	
DC	09-JUL-2001 (first entry)
DE	Nucleotide sequence of the HindIII C fragment of Swinepox virus.
XX	
KW	SPV; vector; pathogen; vaccine; pseudorabies; ds.
XX	
OS	Swinepox virus.
XX	
FT	Key
FT	Location/Qualifiers
FT	CDS
FT	3852..4226
FT	/tag- a
FT	/note- "encodes AAB68229"
FT	4585..4887
FT	/tag- b
FT	/note- "encodes AAB68230"
FT	5131..5310
FT	/tag- c
FT	/note- "encodes AAB68231"
FT	5760..5912
FT	/tag- d
FT	/note- "encodes AAB68232"
FT	6786..7130
FT	/tag- e
FT	/note- "encodes AAB68233"
FT	10148..10513
FT	/tag- f
FT	/note- "encodes AAB68234"
XX	
PN	US6217882-B1.
PD	17-APR-2001.
XX	
PF	26-APR-1999; 99US-0299268.
XX	
PR	14-SEP-1994; 94US-0307499.
PR	21-APR-1989; 89US-0342212.
PR	02-JUL-1992; 92US-0908241.
PR	28-JUL-1997; 97US-0901127.
PR	29-JUN-1992; 92US-0908630.
XX	
PA	(UYFL) UNIV FLORIDA RES FOUND INC.
XX	
PI	Moyer RW, Vinuela E, Glibbs EPT;
DR	WPI: 2001-289820/30.
XX	P-PSDB: AAB68229, AAB68230, AAB68231, AAB68232, AAB68233, AAB68234.
PT	New recombinant swine poxvirus vector, useful in diagnostic,
PT	therapeutic or prophylactic compositions, e.g. as a vaccine against
FT	African swine fever virus, porcine parvovirus, swine influenza, or
XX	especially against pseudorabies -
PS	Claim 8; Fig 2; 116pp; English.
XX	
CC	The present sequence represents a HindIII C fragment of Swinepox virus
CC	(SPV). The polynucleotide fragment was used to construct a recombinant
CC	vector. The vector comprises a heterologous nucleotide sequence encoding
CC	a protein from a selected pathogen inserted into, or replacing, all or a
CC	portion of a swinepox virus gene, which is not essential to replication
CC	of the virus in a host cell. The SPV vector is useful in diagnostic,
CC	therapeutic or prophylactic compositions. In particular, the vector is
CC	useful as a vaccine or a therapy against a selected pathogen,
CC	particularly against pseudorabies. The vector is also useful in
CC	therapeutic or vaccine compositions against TGEV (undetined), African
CC	swine fever virus, porcine parvovirus, swine influenza, hog cholera or
CC	other bacterial pathogens.
XX	
SO	Sequence 14176 BP; 4820 A; 2231 C; 1639 G; 5486 T; 0 other;
Query Match	12.9%; Score 133.6; DB 22; Length 14176;
Best Local Similarity	49.0%; Pred. No. 7.2e-21;

[illegible]


```

FT exon 1199..4225
XX /*tag- b
XX MO8601802-A.
XX 27-MAR-1986.
XX 11-SEP-1985; 85WO-0006960.
XX 11-SEP-1984; 84AU-0007067.
XX 11-SEP-1984; 84AU-0007066.
XX 10-SEP-1985; 85AU-0047326.
XX (HALL-) HALL INST MED RES.
XX
XX Kemp DJ, Anders R, Coppel RL, Brown G, Saint RB, Cowman AF;
XX WPI: 1986-094065/14.
XX P-PSDB; AAP60569.
XX
XX DNA coding for Plasmodium falciparum antigens - expressing
XX poly-peptide(s) having antigenicity of RESA or FIRA antigens of P
XX falciparum
XX
XX Claim 4; Fig 1; 55pp; English.
XX
XX The inventors claim a novel DNA molecule which comprises a
XX nucleotide sequence corresp. to all or a portion of the base
XX sequence coding RESA (AAN60472) or FIRA (AAN60473). RESA and FIRA have
XX antigenicity suitable for providing protective immunity against
XX Plasmodium falciparum malarial infections.
XX
XX Sequence 4590 BP; 1933 A; 437 C; 673 G; 1547 T; 0 other;
SQ
Query Match 4.6%; Score 47.6; DB 7; Length 4590;
Best Local Similarity 44.1%; Pred. No. 0.24;
Matches 200; Conservative 0; Mismatches 254; Indels 0; Gaps 0;
QY 569 AAAATGCTAAAGTGAATACCAAAAGATACACACCTACAGTGAAGTAAAGGGTAAAT 628
DB 3635 AAAAACCAAAATGAAATGTACCAAGAACATGTAACAATATGCTGAAGAAATGTAGAA 3694
QY 629 GAGTTAGAGATGCTGAACATGACTGCTGAAATGACAGTAAATTCATTACCTCTCTGAC 688
DB 3695 CATGATGCTGAAGAAATGTAGAACATGATGCTGAAGAAATGTGAACATGATGCTGAA 3754
QY 689 GTAATTACTAGTGTAGAAAGCGAATTTAAAGTGAATATTAATATGTATTAACGA 748
DB 3755 GAAATGTAGACATGATGCTGAAGAAATGTAGAACATGATGCTGAAGAAATGTAGAA 3814
QY 749 AGATTAATCCAGAAATGGGGAGAAATCCGATTATGAGCCAGAGAGCCAGTTTCCA 808
DB 3815 GAAATGTTGAAGATGAAGAAATGTAGAAAGAAATGTGAAGAAATGTAGAAAGAA 3874
QY 809 TCGAATATTTAAAGATTAAGATGAACATATAGTTTAAAGATTTAGTACTAGCA 868
DB 3875 AATGTTGAAGATGAAGAAATGTAGAAAGAAATGTAGAAAGAAATGTAGAAAGAAAT 3934
QY 869 ACATCAAAATGAGTAGTCACTAGTATGTTGTTTCCATGACACTTTAGAACGCA 928
DB 3935 GTTGAAGAAATGTTGAAGAAATGTGAAGAAATGTGAAGAAATGTGAAGAAAT 3994
QY 929 GTTTAATCTGTTCTGAAGATGCAATGAGAGCTATAGCCACCTATATGAAAGCA 988
DB 3995 GTTGAAGATATGATGAGAAATGTTGAAGAAATGTGAAGAAATGTGAAGAAATGTA 4054
QY 989 GAAGAAGAGAGTGAAGAGAGTGAAGAGAG 1022
DB 4055 GAAGAAGATGTTGAAGAAATGTGAAGAAATG 4088

```

```

ID AAT05868 standard; DNA; 3399 BP.
XX
XX AAT05868;
AC
XX 14-AUG-1996 (first entry)
XX
XX Chicken leucocytozoan DNA encoding immunogenic protein for vaccines.
DE
XX Chicken leucocytozoan; immunogen; recombinant vaccine; protection;
XX immunisation; vaccination; ss.
XX
XX Chicken leucocytozoan.
OS
XX
XX Key Location/Qualifiers
XX CDS 1..3399
XX /*tag= a
XX /*tag= b
XX misc-feature 1150..3218
XX /*tag= b
XX /note= "fragment referred to in the claims, for
XX use as insert in a recombinant vaccine
XX against chicken leucocytozoan disease"
XX
XX JP07284392-A.
XX
XX 31-OCT-1995.
XX
XX 19-APR-1994; 94JP-0080643.
XX
XX 19-APR-1994; 94JP-0080643.
XX
XX (DOBU-) DOBUTSUVO SEIBUTSUGAKUTERI SEIZAI KYOKAI.
XX (KITA) KITASATO KENKYUSHO SH.
XX
XX WPI: 1996-006311/01.
XX P-PSDB; AAR97866.
XX
XX Chicken leucocytozoan immunogenic protein - used in a recombinant
XX vaccine against chicken leucocytozoan disease
XX
XX Claim 6; Page 6-9; 35pp; Japanese.
XX
XX AAT05868 encodes a chicken leucocytozoan immunogenic protein, this DNA
XX or a fragment of it can be used in a recombinant vaccine to immunise
XX against chicken leucocytozoan disease. The DNA is used in a vector
XX and operatively linked to an expression regulatory sequence as in
XX standard practice.
SQ
Sequence 3399 BP; 1577 A; 508 C; 798 G; 516 T; 0 other;
Query Match 4.6%; Score 47.2; DB 17; Length 3399;
Best Local Similarity 43.8%; Pred. No. 0.28;
Matches 205; Conservative 0; Mismatches 263; Indels 0; Gaps 0;
QY 559 AGATTACCAAAATGCTAAAGTGAATACCAAAAGATACACACCTACAGTGAAGT 618
DB 2601 AGAAGAAAGAAAGAAAGTAAACATGTAAGAAAGAAAGTAAACATGTAAGAAAGAA 2660
QY 619 AACGGTAATGATTAAGAAAGTGAATGATGATGATGATGATGATGATGATGATGAT 678
DB 2661 AAAAGTAACATGTAAGAAAGTGAATGATGATGATGATGATGATGATGATGATGAT 2720
QY 679 CCGTCTGACGTAATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 738
DB 2721 TGAGGAAGAAAGAAAGAAAGTGAAGAAAGTGAAGAAAGTGAAGAAAGTGAAGAA 2780
QY 739 TGTTAAGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 798
DB 2781 AGAGGAAGAAAGAAAGTGAAGAAAGTGAAGAAAGTGAAGAAAGTGAAGAAAGTGA 2840
QY 799 AGGTTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 858
DB 2841 AGAAGAAAGAAAGTGAAGAAAGTGAAGAAAGTGAAGAAAGTGAAGAAAGTGAAGAA 2900

```

RESULT 13
AAT05868

OY		859	AGTACGTACAACATCAAAAAATGAGTAGTCACACTACTATATGTGGTTTCCATGACACTTT	918
Db		2901	AACACATTAAGAAGAAAGAAAAGTAAGTAAACATCATGAAGAAGAAAAGTAACACATGA	2966
OY		919	AGAACGCCAAGTTATTACTGTTCTTGGAAGATGCANTGACAGAGCTATACGACCCTATA	978
Db		2961	AGAAAGMAAATAATGTACATATATGAAGAAGAAAGMAAATAAATACATGAAAGAAGA	3022
OY		979	TAGAAAACAGAGAAGAGAAAGGAGGAGAGAGATGAAGAAGCGGAAA	1026
Db		3021	AAAAGTAAACACATGACAGAAAGAAAAGTAAGTAAACATGATGAAGAGAGA	3068
 RESULT 14 ABL/70327/C ABL/70327 standard; DNA; 6012 bp.				
XX	AC	ABL70327:		
XX	DT	01-JUN-2002 (first entry)		
DE		Chemically treated cell signalling DNA sequence#109.		
XX	KW	Cell signalling; cytosine methylation; cell signalling disease;		
XX	KM	Cancer; tumour; cytostatic; ds.		
OS		Unidentified.		
PN		WO200202807-A2.		
PD		10-JAN-2002.		
XX	PF	29-JUN-2001; 2001WO-EP07471.		
PR		30-JUN-2000; 2000DE-1032529.		
XX	PR	01-SEP-2000; 2000DE-1043826.		
PA		(EPIC-) EPIGENOMICS AG.		
PI		Olek A, Piepenbrock C, Berlin K;		
DR		WPI; 2002-154758/20.		
XX		Nucleic acid, useful for diagnosis and therapy of diseases associated		
PT		with cell signalling e.g. cancer, comprises chemically modified genomic		
PT		sequences of genes associated with cell signalling -		
PS		Claim 1; SEQ ID NO 217; 24pp+sequence listing; English.		
XX		The invention relates to a nucleic acid comprising a sequence of at least		
CC		18 bases of a segment of chemically pretreated DNA of genes associated		
CC		with cell signalling. The activity of the modified sequences of the		
CC		invention may be described as cytostatic. The object of the invention is		
CC		to provide the chemically modified DNA of genes associated with cell		
CC		signalling, as well as oligonucleotides and/or PNA-oligomers for		
CC		detecting cytosine methylations, as well as a method which is		
CC		particularly suitable for the diagnosis and/or therapy of genetic and		
CC		epigenetic parameters of genes associated with cell signalling. The		
CC		chemically modified DNA provided by the invention is useful for diagnosis		
CC		and therapy of diseases such as solid tumours and cancer. The sequences		
CC		given in records AB1/70111-AB1/70626 represent chemically pre-treated		
CC		genomic DNA's of genes associated with cell signalling.		
CC		Note: The sequence data for this patent is not represented in the printed		
CC		specification, but is based on sequence information supplied by the		
CC		European Patent Office.		
XX		Sequence 6012 bp; 1785 A; 32 C; 958 G; 3237 T; 0 other;		
SQ		Query Match	4.5%; Score 47; DB 24; Length 6012;	
		Best Local Similarity	51.2%; Pred. No. 0.35;	
OY		Matches	110; Conservative 0; Mismatches 105; Indels 0; Gaps 0;	
		414 ACCATATACGGAGATTAAGGTTTACGAAAATGACACATTAAGGTTTTCCCAAGTTGGANA	473	

Db	4716	AACATAAAAAACTTAAAAAAATTTAAAAAAATCTAATTTTAACTCTCTAAATATTTTAA	4657		
OY	474	TGTTAACTGTAAAAAACACCTCTTTGGAAAGATGTAAAACTTATCTAGCCGTTTGAT	533		
Db	4656	TCCTTAAAAAATAAAAAAATAATATTAATAATATTAATATTAATATTCATA	4597		
OY	534	ACATGGATGTTCAATTTAGCTATTTTACCAAAAAATGGCTAAAGTGAAATACCAA	593		
Db	4596	AAATTAACCTTCATTATTTTATTCCTACTAACCAAAACAAAAATTAATAACTTCAACRA	4537		
OY	594	AAGATACACACCTTACAGTGAAGTAACGGTAAAT	678		
Db	4536	TAACTAAAAACCACTTTATATAAAAAAATTTTCAT	4502		
RESULT 15					
AA661274/c					
ID	AA661274	standard; DNA; 6012 BP.			
XX	AA661274;				
XX	29-JAN-2002	(first entry)			
DE	Human gene regulation-associated gene oligonucleotide #229.				
XX					
KW	Human; Gene regulation-associated gene; severe combined immunodeficiency;				
KW	cardiac damage; inflammatory response; Haemophilia; Werner syndrome;				
KW	asthma; HIR syndrome; congenital heart defect; Saethre-Chotzen syndrome;				
KW	renal disease; Preeclampsia; cardiac allograft vascular disease;				
KW	colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour;				
KW	immunostimulant; caditant; antiinflammatory; coagulant; antiasthmatic;				
XX	nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostatic.				
OS	Homo sapiens.				
XX					
PN	WO20017375-A2.				
XX					
PD	18-OCT-2001.				
XX					
PF	06-APR-2001; 2001WO-EP03968.				
XX					
PR	06-APR-2000; 2000DE-1019058.				
PR	07-APR-2000; 2000DE-1019173.				
PR	30-JUN-2000; 2000DE-1032529.				
XX	01-SEP-2000; 2000DE-1043826.				
PA	(EPIC-) EPIGENOMICS AG.				
PI	Olek A, Piepenbrock C, Berlin K;				
DR	WPI; 2002-017470/02.				
XX					
PT	New nucleic acid sequences from chemically modified genes associated				
PT	with gene regulation, useful for analysing cytosine methylations for				
PT	diagnosis and therapy of diseases e.g. severe combined immunodeficiency				
PT	disease				
XX					
PS	Disclosure; SEQ ID NO 235; 26bp; English.				
XX					
CC	The invention relates to 224 nucleic acid sequences comprising at least				
CC	18 bases of a chemically pretreated gene associated with gene regulation				
CC	selected from 43 known genes (or complementary sequences). The				
CC	chemical pretreatment converts cytosine bases unmethylated at the				
CC	5-position to uracil or another base with hybridisation behaviour				
CC	dissimilar to cytosine, to enable analysis of cytosine methylations.				
CC	The DNA sequences, oligomers (or sets/arrays) and method are				
CC	useful in the diagnosis of diseases (or predisposition to diseases)				
CC	associated with gene regulation and in therapy of such diseases, by				
CC	enabling analysis of the cytosine methylation patterns of such genes,				
CC	kits are provided. They are especially useful in diagnosis				
CC	and therapy of e.g. severe combined immunodeficiency disease, cardiac				
CC	disorders, haemophilia, solid tumours and cancer, Werner syndrome,				

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 20:17:01 ; Search time 78 Seconds
(without alignments)
4065.433 Million cell updates/sec

Title: US-09-976-605-5

Perfect score: 1034
Sequence: 1 aagctcatgaataagtaa.....agaagacggaaccctcgag 1034

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCPUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	133.6	12.9	1023	1	US-08-307-499-53
2	133.6	12.9	1023	4	US-09-299-268-53
3	133.6	12.9	14176	1	US-08-307-499-1
4	133.6	12.9	14176	1	US-08-307-499-14
5	133.6	12.9	14176	4	US-09-299-268-1
6	133.6	12.9	14176	4	US-09-299-268-14
7	59.8	5.8	7218	1	US-08-232-463-14
8	42	4.1	1956	4	US-08-559-8968-1
9	40.6	3.9	4163	4	US-09-004-838-70
10	40.2	3.9	663	4	US-08-998-416-191
11	39.4	3.8	662	4	US-08-998-416-185
12	39	3.8	711	4	US-08-998-416-786
13	39	3.8	724	4	US-08-998-416-683
14	39	3.8	732	4	US-08-998-416-1036
15	39	3.8	828	4	US-08-998-416-538
16	38.4	3.7	1158	4	US-09-134-001C-851
17	38.2	3.7	19124	2	US-08-487-826B-13
18	37.6	3.6	834	4	US-08-998-416-305
19	37.2	3.6	665	4	US-08-998-416-937
20	37.2	3.6	4285	4	US-09-410-464-1
21	37	3.6	3808	2	US-08-417-210A-79
22	36.8	3.6	1431	4	US-09-134-001C-1621
23	36.6	3.5	701	4	US-08-998-416-701
24	36.6	3.5	854	4	US-08-998-416-534
25	36.6	3.5	860	4	US-08-998-416-287
26	36.6	3.5	14507	3	US-08-785-150-1
27	36.6	3.5	14507	4	US-09-660-299-1

28	36.6	3.5	14507	4	US-09-435-377-1	Sequence 1, Appl
29	36	3.5	658	4	US-08-998-416-595	Sequence 595, App
30	36	3.5	3891	1	US-08-480-604A-27	Sequence 27, Appl
31	36	3.5	3891	2	US-08-405-496A-27	Sequence 27, Appl
32	36	3.5	3891	4	US-08-915-136-27	Sequence 27, Appl
33	35.8	3.5	2075	1	US-08-238-163-3	Sequence 3, Appl
34	35.6	3.4	84495	4	US-09-797-906-3	Sequence 334, App
35	35.4	3.4	986	4	US-09-072-596-334	Sequence 3, Appl
36	35.4	3.4	3395	4	US-09-103-478-3	Sequence 3, Appl
37	35.4	3.4	3395	4	US-09-193-931C-3	Sequence 3, Appl
38	35.4	3.4	5181	1	US-08-257-073-10	Sequence 10, Appl
39	35.4	3.4	5470	1	US-08-441-139-12	Sequence 12, Appl
40	35.4	3.4	5470	6	5196523-5	Patent No. 5196523
41	35.4	3.4	7560	4	US-09-103-478-4	Sequence 4, Appl
42	35.4	3.4	7560	4	US-09-193-931C-4	Sequence 4, Appl
43	35.2	3.4	1194	4	US-08-929-329-3	Sequence 3, Appl
44	35	3.4	1236	2	US-08-741-134-5	Sequence 5, Appl
45	35	3.4	4766	5	PCT-US93-07261-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-307-499-53
Sequence 53, Application US/08307499
Patent No. 5651972
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Vi uela, Eladio
APPLICANT: Gibbs, E.P.J.
TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: U.S.A.
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,499
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,241
FILING DATE: 1-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,630
FILING DATE: 29-JUN-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/342,212
FILING DATE: 21-APR-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF35.1.FWCC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 1023 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

Db 754 ATAGAAATGAGTGAAGCAAGCTAGATGAGATTAATAAATCTCCAGAAACGAGTAACTCTTACA 695
Qy 324 ---CGCTTCATTAATCACTGGGCTGTTATGAAACAGGATTAATTTGGTAGTTAGGGT 380
Db 694 AGACTATGTCCTTACCAATTTGATGTACTACTAGACAACTTCAAGTAAATTTGGCTT 635
Qy 381 ATGTAGAAAGCGCCAGCAAGCCGTTGCGCATACCATACAGAGATTAAGTAAAGTTTACGA 440
Db 634 ATGTACTGTAGGTGATTAATATATAGACAGATTCGACCCCAAGAAATAAACGCTTTAGTA 575
Qy 441 AAATGACACATTAAGGTTTCCCAAGTTGGATGTTAACTGTAAAAAACAACCTTTTGA 500
Db 574 AAGTATAGACAGTACATTTCCAAAGGTAGGAATGTTAACTGTAACTCAACAACTGGG 515
Qy 501 AAGATGTAAAAACTTATCTAGCGGCTTTGAATACATGAGATGTTCACTATTTAGT 580
Db 514 AAGCTGTATGGAACATCTTGATCATGTTAATCATTAACATGTCCTTTACAGCGGATG 455
Qy 561 ATTTCACAAAATGCTTAAAGGTGAATACCAAAAGATACACACCTACAGTAAAGTAA 620
Db 454 ATTATTTAAATTTCTAGGGAATATATAGATTAAGCCAGTTAAGCCCTACTGTACAGTTA 395
Qy 621 CGGATATGAGTTAGAGATGATGATACATGACTCTTGATGACAGTAAATTTCACTTACC 680
Db 394 CAGGAATTTGAAGGAGGGA---TAACTCTACATGATGATACCACTTTGATTAATCATTTATC 338
Qy 681 CTCCTGACGTAAATTAATTAAGTGAAGCAAGCAATTTTAAAGTGAATTAATTAATG 740
Db 337 CGTGTGCGTGGCTGTTAAATGATTAATCAATCGAGACTTGGCTCGGAGTATCGTTAG 278
Qy 741 TTAAAGGAATATCTATCCAGATGGGGGAGAAAATCCGTTATGAGCCAGGAGACGAG 800
Db 277 ATCCG-----TACGTAATGAATGCTTCCTGATACGACTATCAACCGGTGAACAG 224
Qy 801 GTTTTCATGGAATATTAATAAAGATTAAGATCAACATTAATTAATTAATTAATTAATG 860
Db 223 GATATCGGACTATTAATGAGATGATGATGATTAATTTATTTACTATCTACCTTAGG 164
Qy 861 TACGTACACATCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 920
Db 163 TTATGTACCAATCATGCTTAATGATGATGATGATGATGATGATGATGATGATGATGATG 104
Qy 921 AAGCGCAAGTTTAACTGT 940
Db 103 AACCAAGCATATTAATGATGT 84

RESULT 4

US-08-307-499-14
Sequence 14, Application US/08307499
Patent No. 5651972
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Vi uela, Eladio
APPLICANT: Gibbs, E.P.J.
TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: U.S.A.
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,499
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,241
FILING DATE: 1-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,630
FILING DATE: 29-JUN-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/342,212
FILING DATE: 21-APR-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF35.1.FWCCI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 14176 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 138..1460
FEATURE:
NAME/KEY: CDS
LOCATION: 2456..2659
FEATURE:
NAME/KEY: CDS
LOCATION: 2809..3030
FEATURE:
NAME/KEY: CDS
LOCATION: 3070..3330
FEATURE:
NAME/KEY: CDS
LOCATION: 3356..4180
FEATURE:
NAME/KEY: CDS
LOCATION: 4392..5894
FEATURE:
NAME/KEY: CDS
LOCATION: 6171..6398
FEATURE:
NAME/KEY: CDS
LOCATION: 6447..6875
FEATURE:
NAME/KEY: CDS
LOCATION: 6928..7431
FEATURE:
NAME/KEY: CDS
LOCATION: 7454..7858
FEATURE:
NAME/KEY: CDS
LOCATION: 7895..8155
FEATURE:
NAME/KEY: CDS
LOCATION: 8215..8682
FEATURE:
NAME/KEY: CDS
LOCATION: 8715..9539
FEATURE:
NAME/KEY: CDS
LOCATION: 9562..10272
FEATURE:
NAME/KEY: CDS
LOCATION: 10316..11908
FEATURE:
NAME/KEY: CDS

100

LOCATION: 4392..5894
 FEATURE: CDS
 NAME/KEY: 6171..6398
 LOCATION: CDS
 NAME/KEY: 6447..6875
 LOCATION: CDS
 NAME/KEY: 6928..7431
 LOCATION: CDS
 NAME/KEY: 7454..7858
 LOCATION: CDS
 NAME/KEY: 7895..8155
 LOCATION: CDS
 NAME/KEY: 8215..8682
 LOCATION: CDS
 NAME/KEY: 8715..9539
 LOCATION: CDS
 NAME/KEY: 9562..10272
 LOCATION: CDS
 NAME/KEY: 10316..11908
 LOCATION: CDS
 NAME/KEY: 11971..12780
 LOCATION: CDS
 NAME/KEY: 12829..13107
 LOCATION: CDS
 NAME/KEY: 13149..14171
 LOCATION: CDS
 US-09-299-268-14

Query Match 12.9% Score 133.6; DB 4; Length 14176;
 Best Local Similarity 49.0%; Pred. No. 3.4e-25;
 Matches 451; Conservative 0; Mismatches 454; Indels 15; Gaps 3;

27 TTAGACATGTGTACAGTTTGTACATGATCTTAAATATATATATCTGTACGT 86
 13183 TTACAGCATATGTATAGATGCTTCCGATTTCTAGATACATATATACATTTACAG 13242
 87 TAAAGATTAATGGTTATACATGAGTATTTTACATCATTTACAGATCAGTATAGTAA 146
 13243 ATGATTAATCATGATATGATGCTTCCGATTTCTAGATACATATATACATTTACAG 13302
 147 CGAATAATATCATATATACAGCAAGATACAGCAAGATTAATTTAG36CTGATTTGT 206
 13303 GTTTTAAATCTAAATGAGCAGACAGAGCAAGCAAGATTAAGAAATGACCAACATGTT 13362
 207 TTAATATTTCTAGAGTCCCAACAGCAAGTAAAGATTAACCTTAACTTTGTGATTT 266
 13363 TTAATGAGCATAGATTTGATATTTCCGAAAAATATATATATTTATTTTGTGCTAA 13422
 267 CTTTATGAAAGAACTTTAGAGAAATTAATTAAGATTAAGCAAAACTACTT--- 323
 13423 ATGATATGAGTAAAGCGTATGATGATTAATTAATTAATTAATTAATTAATTTCCGTT 13482
 324 ---CGCTTCAATTAATCTAGCTGGGTGTTATGAAACAGATTTATTTTGTGATTTGGGT 380
 13483 AGACTATGCTTCTGCAATTTGATGATGATTAAGCAACTCAATTAATTTCCGTT 13542
 381 ATGTAGAAAGCGCAAGCGATGCGCAATTAACATACAGAGATTAAGGTTTACGA 440
 13543 ATGTACTGTAGTGTATATATGATGACAGATTTGACCCCAAGATTAAGCGTTTACGA 13602
 441 AATGACACATTAAGGTTTCCCAAGGTTGGAATTTAACTGTAATAAAACACTGTTTGA 500

13603 AAGTTAGATCAGTACATTTCCAAAGGTAGGAATGTTAACTGTTAAATCAACACATCGG 13662
 501 AAGATGTAATAAATCTATCTAGCGGTTTGAATACATGATGTTCAATTTAGCTTTAG 560
 13663 AAGCTGTATGGAACATCTTGGATCATGTTACATTTAATGATGATGATGATGATGATG 13722
 561 ATTACCAAAAAATGCTAAAGGTAAATATACCAAAAGATTAACACACTACAGTAAATGAA 620
 13723 ATTATTAATAAATTTCTAAGGATATATATATGATTAAGCAGTTAAGCTACGTTTACATTA 13782
 621 CGGTAATGATTTAGAGATGTTAATGATGATGATGATGATGATGATGATGATGATGATG 680
 13783 CAGGAATTAAGAGGAGA---TAATCTACATTTGATGATGATGATGATGATGATGATGATG 13839
 681 CTCTGACGTAAATTTACTAGATGATGATGATGATGATGATGATGATGATGATGATGATG 740
 13840 CGTGTGCGGTGCTGTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 13899
 741 TTAACGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 800
 13900 ATCCG-----TACGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 13953
 801 GTTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 860
 13954 GATATCCGACTATATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 14013
 861 TACGTACATCAATCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 920
 14014 TTATGTAACCAATCATATGCTTAATGATGATGATGATGATGATGATGATGATGATGATGATG 14073
 921 AAGCGCAAGTTTAACTGTTGT 940
 14074 AACCAAGCATATATATGATGT 14093

RESULT 7
 US-08-232-463-14/C
 ; Sequence 14, Application US/08232463
 ; Patent No. 5670367
 ; GENERAL INFORMATION:
 ; APPLICANT: DORNER, F.
 ; APPLICANT: SCHREIFLINGER, F.
 ; APPLICANT: FALKNER, F. G.
 ; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 1800 Diagonal Road, Suite 500
 ; CITY: Alexandria
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22313-0299
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentln Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/232.463
 ; FILING DATE:
 ; PRIORITY APPLICATION DATA:
 ; PRIOR APPLICATION NUMBER: US/07/935.313
 ; FILING DATE:
 ; APPLICATION NUMBER: EP 91 114 300.6
 ; FILING DATE: 26-AUG-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BENT, Stephen A.
 ; REGISTRATION NUMBER: 29,768
 ; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 836-9300
 ; TELEFAX: (703) 683-4109


```

1      RESULT 11
2      US-08-998-416-185/c
3      : Sequence 185 Application US/08998416
4      : Patent No. 6239264
5      :
6      : GENERAL INFORMATION:
7      :
8      : APPLICANT: Philippsen, Peter
9      : APPLICANT: Pohlmann, Rainer
10     : APPLICANT: Steiner, Sabine
11     : APPLICANT: Mohr, Christine
12     : APPLICANT: Wendland, Jürgen
13     : APPLICANT: Knechtel, Philipp
14     : APPLICANT: Reibschuinge, Corinne
15     :
16     : TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPHITII
17     : TITLE OF INVENTION: AND USUS THERIOF
18     :
19     : NUMBER OF SEQUENCES: 1152
20     :
21     : CORRESPONDENCE ADDRESS:
22     :
23     : ADDRESSEE: No. 6239264artis Corporation
24     : STREET: 3054 Cornwallis Road
25     : CITY: Research Triangle Park
26     : STATE: No. 62392644th Carolina
27     : COUNTRY: USA
28     : ZIP: 27709
29     :
30     : COMPUTER READABLE FORM:
31     : MEDIUM TYPE: Floppy disk

```

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/998,416
 FILING DATE: 24-DEC-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: CH 0016/97
 FILING DATE: 31-DEC-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Meigs, J. Timothy
 REGISTRATION NUMBER: 38,241
 REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-541-8587
 TELEFAX: 919-541-8689
 INFORMATION FOR SEQ ID NO: 185:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 662 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: PAG1073UP
 US-08-998-416-185

Query Match 3.8%; Score 39.4; DB 4; Length 662;
 Best Local Similarity 46.1%; Pred. No. 0.26;
 Matches 167; Conservative 0; Mismatches 192; Indels 3; Gaps 1;

QY 18 TATATATTTTGGACAAATTTAGACAGTTTGTACATGATTTAAATATATATATA 77
 DB 602 TATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 543
 QY 78 CTGTTCAGTTAAAGTAATGGGTATACAGAGAGATTTTACGATCTTACAAAGATC 137
 DB 542 TAGATTTAAGTATCTTAAATATATATATATATATATATATATATATATATAT 483
 QY 138 AGTTACTAAGCAAAATATCATATTAACCAAGAACTAGACAGCAAGCAATTTTAAAGG 197
 DB 482 AATTTAAGGTGACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 423
 QY 198 CTGATGTTTATATATTTCTAGAGTCCCAACAGCCAGGTAACGAT--TACAATTTA 254
 DB 422 AAGGTACATTTATTA 363
 QY 255 ACTTTGGTATCTTAAATGAAGAAGAACTTTAGAAAGAAATTAATTAATTAATTA 314
 DB 362 ATATATATATACACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 303
 QY 315 AATCTACCTCGCTTCAATTAATCACTGGGTATATGAAGAAAGAGATTTATTTGGAGTT 374
 DB 302 TTAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTCTATT 243
 QY 375 AT 376
 DB 242 AT 241

RESULT 12
 US-08-998-416-786/c
 Sequence 786, Application US/08998416
 Patent No. 6239264
 GENERAL INFORMATION:
 APPLICANT: Philippesen, Peter
 APPLICANT: Pohlmann, Rainer
 APPLICANT: Steiner, Sabine
 APPLICANT: Mohr, Christine
 APPLICANT: Wendland, Jurgen
 APPLICANT: Knechtle, Philipp
 APPLICANT: Redischung, Corinne

TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPPII
 TITLE OF INVENTION: AND USES THEREOF
 NUMBER OF SEQUENCES: 1152
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 6239264rtis Corporation
 STREET: 3054 Cornwallis Road
 CITY: Research Triangle Park
 STATE: No. 6239264th Carolina
 COUNTRY: USA
 ZIP: 27709
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/998,416
 FILING DATE: 24-DEC-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: CH 0016/97
 FILING DATE: 31-DEC-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Meigs, J. Timothy
 REGISTRATION NUMBER: 38,241
 REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-541-8587
 TELEFAX: 919-541-8689
 INFORMATION FOR SEQ ID NO: 786:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 711 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: PAG1504UP
 US-08-998-416-786

Query Match 3.8%; Score 39; DB 4; Length 711;
 Best Local Similarity 45.9%; Pred. No. 0.34;
 Matches 172; Conservative 0; Mismatches 200; Indels 3; Gaps 1;

QY 5 TTCAATGAATTAAGTAAATTTATTTAGCACAATTTGACAGTTTGTACATGCAATTA 64
 DB 616 TTACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 557
 QY 65 AATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 124
 DB 556 GATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 497
 QY 125 CATTAACAAGTATCACTAGTACGAAATATATATATATATATATATATATATATAT 184
 DB 496 GGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 437
 QY 185 GTAAATTTAGGCTGATTTGTTAATTTTCTAGAGTCCCAACAGCCAGGTAACGAT 244
 DB 436 AATAATATTAATGAAGAGACATTAATTAATTAATTAATTAATTAATTAATTAATTA 317
 QY 245 ---TCAACTTTAACTTTTGTATCTTAATGAAGAAAGAACTTTAGAAAGAAATTAATA 301
 DB 376 TTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 317
 QY 302 AAGCATGCAAAAAGTACTTCCCTTCAATTAATCACTGGGTATATGAAGAGATTA 361
 DB 316 AAAAATGGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 257
 QY 362 TTATTTGGTACTAT 376
 DB 256 TAATTTCTATTAT 242


```

1      RESULT 13
2      US-08-998-416-683/C
3      ; Sequence 683, Application US/08998416
4      ; Patent No. 6239264
5      ;
6      ; GENERAL INFORMATION:
7      ; APPLICANT: Philippson, Peter
8      ; APPLICANT: Pohlmann, Rainer
9      ; APPLICANT: Steiner, Sabine
10     ; APPLICANT: Mohr, Christine
11     ; APPLICANT: Wendland, Jurgen
12     ; APPLICANT: Knechtle, Philipp
13     ; APPLICANT: Reibischung, Corinne
14     ;
15     ; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSTYLLII
16     ;
17     ; TITLE OF INVENTION: AND US$S THEREOF
18     ;
19     ; NUMBER OF SEQUENCES: 1152
20     ;
21     ; CORRESPONDENCE ADDRESS:
22     ; ADDRESSEE: No. 6239264artis Corporation
23     ; STREET: 3054 Cornwallis Road
24     ; CITY: Research Triangle Park
25     ; STATE: No. 6239264th Carolina
26     ;
27     ; COUNTRY: USA
28     ;
29     ; ZIP: 27709
30     ;
31     ; COMPUTER READABLE FORM:
32     ; MEDIUM TYPE: Floppy disk
33     ; COMPUTER: IBM PC compatible
34     ; OPERATING SYSTEM: PC-DOS/MS-DOS
35     ; SOFTWARE: Patentin Release #1.0, Version #1.30
36     ;
37     ; CURRENT APPLICATION DATA:
38     ; APPLICATION NUMBER: US/08-998,416
39     ; FILING DATE: 24-DEC-1997
40     ; CLASSIFICATION: 435
41     ;
42     ; PRIOR APPLICATION DATA:
43     ; APPLICATION NUMBER: CH 0016/97
44     ; FILING DATE: 31-DEC-1996
45     ; ATTORNEY/AGENT INFORMATION:
46     ; NAME: Meigs, J. Timothy
47     ; REGISTRATION NUMBER: 38,241
48     ;
49     ; TELECOMMUNICATION INFORMATION:
50     ; TELEPHONE: 919-541-8587
51     ; TELEFAX: 919-541-8689
52     ;
53     ; INFORMATION FOR SEQ ID NO: 683:
54     ; SEQUENCE CHARACTERISTICS:
55     ; LENGTH: 724 base pairs
56     ; TYPE: nucleic acid
57     ; STRANDEDNESS: single
58     ; TOPOLOGY: linear
59     ; MOLECULE TYPE: DNA (genomic)
60     ; ORIGINAL SOURCE:
61     ; ORGANISM: PAG1453RP
62     ;
63     ;
64     ; US-08-998-416-683

```

[illegible][illegible]

```

US-08-998-416-1036/c
: Sequence 1036, Application US/08998416
: Patent No. 6239264
: GENERAL INFORMATION:
:   APPLICANT: Philippsen, Peter
:   APPLICANT: Pohlmann, Rainer
:   APPLICANT: Steiner, Sabine
:   APPLICANT: Mohr, Christine
:   APPLICANT: Wendland, Jürgen
:   APPLICANT: Knechtle, Philipp
:   TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSPYITII
:   TITLE OF INVENTION: AND USES THEREOF
:   NUMBER OF SEQUENCES: 1152
: CORRESPONDENCE ADDRESS:
:   ADDRESSEE: No. 6239264artis Corporation
:   STREET: 3054 Cornwallis Road
:   CITY: Research Triangle Park
:   STATE: No. 6239264ch Carolina
:   COUNTRY: USA
:   ZIP: 27709
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: Floppy disk
:   COMPUTER: IBM PC compatible
:   OPERATING SYSTEM: PC-DOS/MS-DOS
:   SOFTWARE: Patentin Release #1.0, Version #1.30
:   CURRENT APPLICATION DATA:
:     APPLICATION NUMBER: US/08/998,416
:     FILING DATE: 24-DEC-1997
:     CLASSIFICATION: 435
:     PRIOR APPLICATION DATA:
:       APPLICATION NUMBER: CH 0016/97
:       FILING DATE: 31-DEC-1996
:       ATTORNEY/AGENT INFORMATION:
:         NAME: Meigs, J. Timothy
:         REGISTRATION NUMBER: 38,241
:         REFERENCE/DOCKET NUMBER: PF/5-30306/A/GC1976
:         TELECOMMUNICATION INFORMATION:
:           TELEPHONE: 919-541-8587
:           TELEFAX: 919-541-8689
:       INFORMATION FOR SEQ ID NO: 1036:
:         SEQUENCE CHARACTERISTICS:
:           LENGTH: 732 base pairs
:           TYPE: nucleic acid
:           STRANDEDNESS: single
:           TOPOLOGY: linear
:         MOLECULE TYPE: DNA (genomic)
:         ORIGINAL SOURCE:
:           ORGANISM: PG16330P
US-08-998-416-1036

```

Query Match	3.8%;	Score 39;	DB 4;	Length 722;
Best Local Similarity	45.9%;	Pred. No. 0.34;		
Matches	172;	Conservative	0;	Mismatches 200; Indels 3; Caps 1
Oy	5	TTTCATCAAAAGTATATATTTTATGACCAATGTGACAGCTTTGACACGATCAACTT	64	
Db	615	TTTCCTATTTATTAATATATTTTATATATATATATATATATATATATATATATATCTTAA	556	
Oy	65	AAATATATATTAATCTGTTACGTTAAAGATATAGCGTTATTCAGATGAGATATTTTCAGAT	124	

```

; ORGANISM: PAG1375RP
US-08-998-416-538
Query Match
Best Local Similarity 45.98; Score 39; DB 4; Length 828;
Matches 172; Conservative 0; Mismatches 200; Indels 3; Gaps 1;

QY 5 TTCAATGATTAAGTTAAATTAATTTAGACAAATTTGACAGTTTGTACTGCATTAACCTTA 64
DB 615 TTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 556
QY 65 AAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 124
DB 555 GATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 496
QY 125 CATTACAAAGATCAGTTAGTAACGAAATATCATATTAACCAAGAACTGACAGGAAAC 184
DB 495 GGTAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 436
QY 185 GTAAATTTTAAAGGCTGATTTGTTTAATTTCTAGAGATCCACACGCCAGCTAACGAT 244
DB 435 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 376
QY 245 ---TAAACTTTAACTTTGTTTGTATTTCTTAATGAAGAAGAACTTTAGAAATTAATAA 301
DB 375 TTATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 316
QY 302 AACGATAGCACAATAACTCTGCTTCATTATACACTGGGTGTTATGAACAGATTA 361
DB 315 AAAAATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAG 256
QY 362 TTATTTGGTAGTTAT 376
DB 255 TAATTTCTTATTTAT 241

```

```

RESULT 15
US-08-998-416-538/c
; Sequence 538, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Redischung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSTII
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; City: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 538:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 828 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:

```

```

; ORGANISM: PAG1375RP
US-08-998-416-538
Query Match
Best Local Similarity 45.98; Score 39; DB 4; Length 828;
Matches 172; Conservative 0; Mismatches 200; Indels 3; Gaps 1;

QY 5 TTCAATGATTAAGTTAAATTAATTTAGACAAATTTGACAGTTTGTACTGCATTAACCTTA 64
DB 615 TTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 556
QY 65 AAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 124
DB 555 GATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 496
QY 125 CATTACAAAGATCAGTTAGTAACGAAATATCATATTAACCAAGAACTGACAGGAAAC 184
DB 495 GGTAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 436
QY 185 GTAAATTTTAAAGGCTGATTTGTTTAATTTCTAGAGATCCACACGCCAGCTAACGAT 244
DB 435 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 376
QY 245 ---TAAACTTTAACTTTGTTTGTATTTCTTAATGAAGAAGAACTTTAGAAATTAATAA 301
DB 375 TTATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 316
QY 302 AACGATAGCACAATAACTCTGCTTCATTATACACTGGGTGTTATGAACAGATTA 361
DB 315 AAAAATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAG 256
QY 362 TTATTTGGTAGTTAT 376
DB 255 TAATTTCTTATTTAT 241

```

Search completed: June 15, 2003, 21:38:11
Job time : 82 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 20:15:21 ; Search time 1497 Seconds

(without alignments)
1186.462 Million cell updates/sec

Title: US-09-976-605-5

Perfect score: 1034

Sequence: 1 aagctcatgataaagtaaa.....agaagacgaacccctgag 1034

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estinu:*
5: em_estov:*
6: em_estopl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62	6.0	1161	BE421968	BE421968 HMW017CF
2	59.8	5.8	1101	17 CNS0039G	AL063921 Drosophila
3	59.8	5.8	1101	17 CNS0039G	AL064091 Drosophila
4	57.4	5.6	1101	17 CNS0182P	AL108811 Drosophila
5	55.8	5.4	938	17 CNS0067J	AL055906 Drosophila
6	53.2	5.1	843	17 CNS00C51	AL055666 Drosophila

7	53.2	5.1	1225	17	CNS0161D	AL106171 Drosophila
8	52.8	5.1	974	17	CNS0017T	AL075432 Drosophila
9	52	5.0	997	17	CNS0050R	AL060767 Drosophila
10	51.8	5.0	538	9	AU053236	AU053236 AU053236
11	51.8	5.0	928	17	CNS000KX	AL071865 Drosophila
12	51.8	5.0	928	17	CNS000EVL	AL069706 Drosophila
13	51.2	5.0	581	17	CNS010P2	AL168128 Tetradon
14	50.8	4.9	385	14	BO596570	BO596570 Pterodon
15	50.6	4.9	1101	17	CNS0006T	AL062049 Drosophila
16	50.2	4.9	928	17	CNS0102F	AL098433 Drosophila
17	49.6	4.8	1101	17	CNS00E07	AL069440 Drosophila
18	49.4	4.8	1101	17	CNS0067Y	AL063008 Drosophila
19	49.2	4.8	734	17	CNS010MP	AL099163 Drosophila
20	49	4.7	909	17	CNS012AT	AL101327 Drosophila
21	49	4.7	1101	17	CNS0039G	AL063921 Drosophila
22	49	4.7	1101	17	CNS0039R	AL063932 Drosophila
23	48.8	4.7	629	13	BU422197	BU422197 Drosophila
24	48.6	4.7	928	17	CNS000KX	AL071865 Drosophila
25	48.6	4.7	987	17	CNS014PQ	AL104456 Drosophila
26	48.2	4.7	888	17	CNS007VQ	AL050896 Drosophila
27	48.2	4.7	1031	17	CNS00C82	AL059139 Drosophila
28	48.2	4.7	1101	17	CNS008X3	AL052544 Drosophila
29	48	4.6	639	17	CNS0170D	AL108367 Drosophila
30	48	4.6	878	17	CNS0187R	AL108993 Drosophila
31	47.8	4.6	1225	17	CNS0161D	AL106171 Drosophila
32	47.8	4.6	500	9	AU087771	AU087771 AU087771
33	47.8	4.6	1101	17	CNS000B8	AL063632 Drosophila
34	47.6	4.6	877	17	AZ51291	AZ51291 ENTPB34QR
35	47.6	4.6	879	17	CNS010TG	AL147405 Anopheles
36	47.6	4.6	908	17	AZ548467	AZ548467 ENTPB30TR
37	47.6	4.6	912	17	AZ551092	AZ551092 ENTPB22TF
38	47.6	4.6	1101	17	CNS00CYH	AL060100 Drosophila
39	47.6	4.6	1101	17	CNS00EPO	AL069493 Drosophila
40	47.6	4.6	1184	13	BM545225	BM545225 AGENCOURT
41	47.4	4.6	945	17	CNS04DOK	AL285149 Tetradon
42	47.4	4.6	1092	17	CNS020K7	AL175636 Tetradon
43	47.4	4.6	1200	17	CNS016EL	AL106647 Drosophila
44	47.2	4.6	961	17	CNS008H1	AL051882 Drosophila
45	47.2	4.6	1101	17	CNS000D1	AL065414 Drosophila

ALIGNMENTS

RESULT 1
BE421968
LOCUS
DEFINITION
HMW017CF.0br ITCB HMW Barley leaf library Hordeum vulgare cDNA
clone HMW017CF.08, mRNA sequence.
BE421968
VERSION
BE421968.1 GI:9419811
KEYWORDS
SOURCE
ORGANISM
Hordeum vulgare.
Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordeum.
1 (bases 1 to 1161)

REFERENCE
AUTHORS
Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier
, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P.,
Herrmann, R.G., Holton, T., Jacquemelin, J.M., Jia, J., Joudrier, P.,
Langridge, P., Lazo, G.R., Lin, J.D., McGuire, P., Ogihara, Y.,
Pechioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M.,
Sorrells, M., Warburton, M. and Wenzel, G.
International Triticeae EST Cooperative (ITEC): Production of
Expressed Sequence Tags for Species of the Triticeae
Unpublished (2000)
CONTACT: Wenzel G
TU Munchen, Lehrstuhl fur Pflanzenbau und Pflanzenzuchtung
Am Hochanger 2, D-85350 Freising-Weihenstephan GERMANY
Fax: 49 08161 71 5173
Email: wenzel@em.phz.agrar.tu-muenchen.de

JOURNAL
COMMENT
International Triticeae EST Cooperative (ITEC)

Db 618 DMTTRDRMDRMAADWTDRKRDWMAFAARARARARARADRETTTKRTTAAW 559
 QY 800 GGTTCATGAGATAATTAAGATGACAAACATATAGTTTACAGATTAA 859
 Db 558 TTAABAAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMA 499
 QY 860 GTACGACACATCAAAAATGAGTACATGATGATGTTTCCATGACACTTA 919
 Db 498 WTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 439
 QY 920 GAAGCGCAAGTTATCTGTTCTGAA 946
 Db 438 TWTWTWMAATTTATTTTWTWMAAA 412

RESULT 3
 CENS003BD 1101 bp DNA linear GSS 03-JUN-1999
 LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #
 DEFINITION BACR08K08 of RPCI-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 AL064091 GI:4941847

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Drosophila melanogaster.
 Drosophila melanogaster.
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 1101)
 Genoscope.
 Direct Submission

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 Evry cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
 Web : www.genoscope.cns.fr
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see http://www.fruitfly.org The BDGP Drosophila
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and
 Aaron Mamoser in Pieter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPCI-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain y2; cn bw sp, the same strain used for the BDGP's
 pl and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
 source
 1. 1101
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone="BACR08K08"
 /clone_1lb="RPCI-98"
 /note="end : TET3"
 Location/Qualifiers

BASE COUNT 395 a 120 c 103 g 334 t 149 others
 ORIGIN

Query Match 5.8%; Score 59.8; DB 17; Length 1101;
 Best Local Similarity 39.1%; Pred. No. 0.023;
 Matches 196; Conservative 45; Mismatches 258; Indels 2; Gaps 1;

QY 239 AACGATCACTTAATTTGGATCTTTATGAAGAACTTTAGAAATTAAT 298
 Db 527 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 586
 QY 239 AAAAAAGATACACAAAAACTCGCTTCATTAAATCAGCGGTGTTAGAAACGCA 358
 Db 587 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 646

QY 359 TTATTATTGGTAGTAAAGGATGATGAGAAACGCCACGCGTTGGCAGATACAT 418
 Db 647 TAATTTTAAATTAATTTTATTTTAAWMAWMAWMAWMAWMAWMAWMAWMAW 706
 QY 419 ACAGAGATTAAGGTTTACGAAATGACACATAAAGGTTTCCAGGTTGATGTTA 478
 Db 707 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 766
 QY 479 ACTGTAAAAACACGCTTGGAAAGATGTAAAAACTTCTAGCGCGTTTGAATACATG 538
 Db 767 ATTATTAATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTA 826
 QY 539 GGATGTCATTAGCTATTGTTTATGATTAACCAAAAAATGCTTAAGGTAAGCAAAAGAT 598
 Db 827 --AATWTAATTAATAATTTNTAATAAATAAATAAATAAATAAATAATATWTAAT 884
 QY 599 ACAACACTACAGTAAGTAACGGGTAATGATGATGAAGATGTAACATGACTCTGAA 658
 Db 885 AAWTTTMAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 944
 QY 659 TGCAGTGAATATCTTTTACCCGCGAGCTAATTAAGTGTGATGATGAACGACAT 718
 Db 945 YTAWMAATWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMA 1004
 QY 719 TTTAAGGTGAATATTAATAT 739
 Db 1005 AATWMAATWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMA 1025

RESULT 4
 CENS0182P 1101 bp DNA linear GSS 26-JUN-1999
 LOCUS Drosophila melanogaster genome survey sequence sp6 end of BAC
 DEFINITION BACN37D10 of DrosBAC library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 AL108611 GI:5629115

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Drosophila melanogaster.
 Drosophila melanogaster.
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 1101)
 Genoscope.
 Direct Submission

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 Submitted (23-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 Evry cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
 Web : www.genoscope.cns.fr
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the European Drosophila Genome Project (EDGP) -
 http://www.edgp.ebi.ac.uk. This Drosophila melanogaster BAC
 library (Dros BAC) was made by Alain Billand at CEPH (Centre
 d'Etude du Polymorphisme Humain) with funding provided by a MRC
 project grant. The DNA was prepared from embryos by Alain Bucheton
 and Genevieve Payan. It has been constructed in the vector
 pBelosBAC11.

FEATURES
 source
 1. 1101
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone="BACN37D10"
 /clone_1lb="DrosBAC"
 /plasmid="pBelosBAC11"
 /note="end : Sp6"
 Location/Qualifiers

BASE COUNT 274 a 268 c 128 g 73 t 358 others
 ORIGIN

Query Match 5.6%; Score 57.4; DB 17; Length 1101;
 Best Local Similarity 19.3%; Pred. No. 0.071;
 Matches 90; Conservative 184; Mismatches 193; Indels 0; Gaps 0;

QY 440 AAATGACACATAAAGTTTCCCAAGGTGGAATGTAATCACTAAAAACACTTTGG 499

[illegible]

	CNS006TJ/C	RESULT 5
		CNS006TJ/C
		LOCUS
		DEFINITION
	Drosophila melanogaster genome survey sequence T7 end of BAC #	
	BACH1411 of RPCI-98 library from Drosophila melanogaster (fruit	
	fly), genomic survey sequence.	
	AL065906	
	GI:4944874	
	GSS.	
	Drosophila melanogaster.	
	Drosophila melanogaster	
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Prelygota;	
	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
	Ephyridae; Drosophilidae; Drosophila.	
	1 (bases 1 to 938)	
REFERENCE	Genoscope.	
AUTHORS	Direct Submission	
TITLE	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :	
JOURNAL	BP 191 91006 EVRY cedex - FRANCE (E-mail : sequefgenoscope.cns.fr	
	- Web : www.genoscope.cns.fr)	
COMMENT	determination of this BAC-end sequence was carried out as part of a	
	collaboration with the Berkeley Drosophila Genome Project (BDGP).	
	The BDGP is constructing a physical map of the Drosophila	
	melanogaster genome using these BACs. For further information	
	please see http://www.fruitfly.org The BDGP Drosophila	
	melanogaster BAC library was prepared by Kazutoyo Osoegawa and	
	Aaron Mammoset in Pieter de Jong's laboratory in the Department of	
	Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,	
	NY. The library is named RPCI-98 and was constructed by partial	
	EcoRI digestion of Drosophila DNA provided by the BDGP from the	
	isogenic strain y2; cn bw sp, the same strain used for the BDGP's	
	p1 and EST libraries. A more detailed description of the library	
	and how to order individual BAC clones, the entire library, or	
	filters for hybridization from the BACPAC Resource Center can be	
	found at http://bacpac.med.buffalo.edu/drosophila_bac.htm .	

FEATURES	Location/Qualifiers
SOURCE	1..938
	/organism="Drosophila melanogaster"
	/db_xref="taxon:7227"
	/clone="BACR14J11"
	/clone_1lb="RPCI-98"

[illegible]

	RESULT 6			
CNS00C0S1/c				
LOCUS				
DEFINITION				
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				

CNS00C0S1 843 bp DNA linear GSS 04-JUN-1999

Drosophila melanogaster genome survey sequence TERT3 out of BAC #
BACR26H19 of RCTI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

AL059666
AL059666.1 GI:4947129
GSS.

Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Epiphytoidae; Drosophilidae; Drosophila.
1 (bases 1 to 843)
Genoscope.
Direct Submissions
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

determination of this BAC end and sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mamoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RCTI-98 and was constructed by partial
isogenic digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2⁺, cn bw ap, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library

TITLE Williams, J., Maeda, M., Takeuchi, I., Ohtani, H. and Tanaka, Y.
JOURNAL Developmental cDNA in Dictyostelium discoideum
COMMENT Unpublished (1998)
Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp
PROJECT = Dictyostelium discoideum cDNA project in Japan.

FEATURES
source location/Qualifiers
1. 538
/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="SLI202"
/clone_lib="Dictyostelium discoideum SL (H.Urushihara)"
/dev_stage="slug"
BASE COUNT 257 a 57 c 123 g 101 t
ORIGIN

Query Match 5.0%; Score 51.8; DB 9; Length 533;
Best Local Similarity 47.6%; Pred. No. 0.99; Indels 0; Gaps 0;
Matches 152; Conservative 0; Mismatches 167; Indels 0; Gaps 0;

QY 706 AGAAGCGACATTTTAAAGGTGAATATTAATGTTTAAACGAGATATCAATCCAGATG 765
DB 220 AGATGATGACGACGATGAGAGATATGATGATATCAATGAGAGATCTTAAATAT 279
QY 766 GGGGAGAAATCCGATTATGAGCCAGAGACCGATTCCATGGAATATTAAGAA 825
DB 280 TGATGCCCAATTTGAAAGATGCAACAGAAATGGGTGATGACCTTGAAAGCATGATGA 339
QY 826 TAAAGTCAACACATATAGTATTAACAGATTTAGTACATCAACATCAAAATGAGTAG 885
DB 340 CGAAG 399
QY 886 TCAACTAGTATGTGTTTCCATGACATCTTGAAGACGCAAGTTTACTTGTCTGA 945
DB 400 TCCACTCATCTCTACTTAAAGAAATCTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 459
QY 946 AGATGCAATGAGAGATGATGACACCTTATATAGAGAGAGAGAGAGAGAGAGAG 1005
DB 460 AGTACCATTTTGAAG 519
QY 1006 AGAGATGAG 1024
DB 520 AGAAG 538

RESULT 11
CNS00DKY 928 bp DNA linear GSS 04-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC #
DEFINITION BACR27A24 of RPI1-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL071865.1 GI:4948170
VERSION AL071865
KEYWORDS GSS.
SOURCE Drosophila melanogaster.
ORGANISM Drosophila melanogaster.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 928)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org/TheBDGP/Drosophila>
melanogaster BAC library was prepared by Kazuhiro Osoegawa and Aaron Mammeter in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPI1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
source location/Qualifiers
1. 928
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACR27A24"
/clone_lib="RPI1-98"
/note="end : 17"

BASE COUNT 262 a 70 c 84 g 321 t 191 others
ORIGIN

Query Match 5.0%; Score 51.8; DB 17; Length 928;
Best Local Similarity 31.9%; Pred. No. 1;
Matches 119; Conservative 81; Mismatches 172; Indels 1; Gaps 1;

QY 12 ATAAGTAATATATTTAGCAATGTTAGCATTTGATCGCAATCACTTAATATTA 71
DB 519 AAAAAAATAAATTTTATTTTAAATATTTTAAATATTTTAAATATTTTAAATATTT 578
QY 72 ATATAGTGTAGTTAAAGATTAATGTTATAGATGAGATTTTACATCAATTA 131
DB 579 ATTWTA-TWTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 637
QY 132 ACGATCGATTAGTACAAATATCATATACAGAGAAATACAGACGAAAGTTAAT 191
DB 638 TWTWTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 697
QY 192 TTAGGCTGATTTGTTAATATTTCTAGAGTCCCGACAGCGAGTAACTTAACT 251
DB 698 AAAAAATTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 757
QY 252 TTAACCTTTGTAATCTTTAATGAGAGAACTTGAAGAAATTAATTAATTAATTA 311
DB 758 NNAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 817
QY 312 CAAAACTACTTCTGCTTCAATATATCTGCGGTATGAGAAAGATTTATTTGTA 371
DB 818 WDDMMRAAKKK 877
QY 372 GTTATGGGTATGT 384
DB 878 TTTTATTTTATTTT 890

RESULT 12
CNS00EVL 1101 bp DNA linear GSS 04-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC:
DEFINITION BACR29B23 of RPI1-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL069706.1 GI:494849
VERSION AL069706
KEYWORDS GSS.
SOURCE Drosophila melanogaster.
ORGANISM Drosophila melanogaster.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
AUTHORS Genoscope.
TITLE Direct Submission

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 20:20:31 ; Search time 186 Seconds

(without alignments)
8049.972 Million cell updates/sec

Title: US-09-976-605-5

Perfect score: 1034
1 aagcttcataagtaagttta.....agaagcaggaacccctcgag 1034

Scoring table: IDENTITY_NTC
Gapop 10.0 , Gapext 1.0

Searched: 1029858 segs, 72403093 residues

Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1034	100.0	1034	US-09-976-605-5	Sequence 5, Appl1
2	986.6	95.4	1017	US-09-976-605-7	Sequence 7, Appl1
3	571.6	55.3	1183	US-09-976-605-3	Sequence 3, Appl1
4	133.6	12.9	1023	US-09-976-605-8	Sequence 9, Appl1
5	44.6	4.3	7195	US-10-239-676-30	Sequence 30, Appl1
6	43	4.2	519	US-09-878-574-4292	Sequence 4292, Ap
7	42	4.1	1956	US-09-351-794A-1	Sequence 1, Appl1
8	42	4.1	402850	US-09-844-653-5	Sequence 5, Appl1
9	41.6	4.0	563	US-09-864-761-13293	Sequence 13293, A
10	41	4.0	2000	US-09-938-842A-3532	Sequence 3532, Ap
11	40.2	3.9	6204	US-10-239-676-190	Sequence 190, App
12	40	3.9	335913	US-09-754-853A-2	Sequence 2, Appl1
13	40	3.9	335913	US-09-754-853A-3	Sequence 3, Appl1
14	39.8	3.8	640681	US-09-790-988-1	Sequence 1, Appl1
15	39.6	3.8	640681	US-09-790-988-1	Sequence 1, Appl1
16	39.2	3.8	28897	US-09-764-877-3897	Sequence 3897, Ap
17	39	3.8	6022	US-10-239-676-80	Sequence 80, Appl1
18	39	3.8	9539	US-10-239-676-51	Sequence 51, Appl1
19	38.8	3.8	465	US-09-918-995-13214	Sequence 13214, A

C 20	38.8	3.8	7906	9	US-10-239-676-97	Sequence 97, Appl1
C 21	38.6	3.7	1503841	9	US-09-946-807-1	Sequence 1, Appl1
C 22	38.6	3.7	1503841	10	US-09-795-668-1	Sequence 1, Appl1
C 23	38.6	3.7	1503841	10	US-09-795-668-1	Sequence 1, Appl1
C 24	38.4	3.7	12465	9	US-10-239-676-31	Sequence 31, Appl1
C 25	38	3.7	3825	12	US-10-051-952-8	Sequence 8, Appl1
C 26	37.8	3.7	2244	7	US-08-781-986A-270	Sequence 270, App
C 27	37.8	3.7	8895	9	US-10-091-438-250	Sequence 250, App
C 28	37.8	3.7	8895	9	US-10-091-438-250	Sequence 250, App
C 29	37.8	3.7	8895	9	US-10-091-438-256	Sequence 256, App
C 30	37.8	3.7	8895	10	US-09-764-883-887	Sequence 887, App
C 31	37.8	3.7	8895	10	US-09-764-883-887	Sequence 887, App
C 32	37.8	3.7	9656	9	US-10-091-438-246	Sequence 937, App
C 33	37.8	3.7	9656	9	US-10-091-438-246	Sequence 937, App
C 34	37.8	3.7	9656	10	US-09-764-883-886	Sequence 886, App
C 35	37.8	3.7	32204	9	US-09-764-883-933	Sequence 255, App
C 36	37.8	3.7	32204	9	US-10-072-349-327	Sequence 327, App
C 37	37.8	3.7	32204	9	US-10-072-349-327	Sequence 327, App
C 38	37.8	3.7	397658	10	US-09-813-320-3	Sequence 3, Appl1
C 39	37.6	3.6	2530	10	US-09-764-877-2332	Sequence 2332, Ap
C 40	37.6	3.6	5979	9	US-10-239-676-18	Sequence 18, Appl1
C 41	37.4	3.6	5935	9	US-10-239-676-133	Sequence 133, App
C 42	37.2	3.6	550	9	US-09-991-936-1334	Sequence 1334, Ap
C 43	37.2	3.6	1569	9	US-09-938-842A-3739	Sequence 3739, Ap
C 44	37.2	3.6	4285	9	US-10-104-580-1	Sequence 1, Appl1
C 45	36.8	3.6	281	10	US-09-864-761-24730	Sequence 24730, A

ALIGNMENTS

RESULT 1
US-09-976-605-5
Sequence 5, Application US/09976605
Patent No. US20020102535A1
GENERAL INFORMATION:
APPLICANT: MCFADEN, GRANT
APPLICANT: ESSANI, KARIM
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND POLYPEPTIDES
FILE REFERENCE: 50082/015002
CURRENT APPLICATION NUMBER: US/09/976, 605
CURRENT FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: US 60/239,354
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1034
TYPE: DNA
ORGANISM: Tanapox virus
US-09-976-605-5

Query Match 100.0%; Score 1034; DB 10; Length 1034;
Best Local Similarity 100.0%; Pred. No. 7.7e-222;
Matches 1034; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAGCTTCATGATAGTTAATATTATTAGACATTTGTACGATGATTAAC 60
DB 1 AAGCTTCATGATAGTTAATATTATTAGACATTTGTACGATGATTAAC 60
OY 61 TTTAAATATATATATATCTGTACGTTAAAGATATGTTATACGATGATTTTA 120
DB 61 TTTAAATATATATATATCTGTACGTTAAAGATATGTTATACGATGATTTTA 120
OY 121 CGATCATTAACAGCATGATTAAGTAAGCAAAATATCAATTAACACCAAACTAGACCG 180
DB 121 CGATCATTAACAGCATGATTAAGTAAGCAAAATATCAATTAACACCAAACTAGACCG 180
OY 181 AAAGTAATTTTGGGCTATTGTTAATATTTCAGAGTCCACACGCGCAGGTAA 240
DB 181 AAAGTAATTTTGGGCTATTGTTAATATTTCAGAGTCCACACGCGCAGGTAA 240

```

QY 241 CGATTACACCTTTTACCTTTGGTATCTTTTAAATGAAGAACTTTAGAGAAATTAATAA 300
    |||
DB 241 CGATTACACCTTTTACCTTTGGTATCTTTTAAATGAAGAACTTTAGAGAAATTAATAA 300
QY 301 AAACGATAGCAGAAAACTACTCTGCTTCATTAATCACTGGGTATGAGAAAGAGATT 360
    |||
DB 301 AAACGATAGCAGAAAACTACTCTGCTTCATTAATCACTGGGTATGAGAAAGAGATT 360
QY 361 ATTATTTGGTATGATGGGTATGATGAGAAAGCGGACGACCGTGGCCGATCCATAC 420
    |||
DB 361 ATTATTTGGTATGATGGGTATGATGAGAAAGCGGACGACCGTGGCCGATCCATAC 420
QY 421 AGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
    |||
DB 421 AGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 481 TGTAAAAAAGCTCTTTGGAAAGATGTAATACTTATAGCGGTTTGAATACATGCG 540
    |||
DB 481 TGTAAAAAAGCTCTTTGGAAAGATGTAATACTTATAGCGGTTTGAATACATGCG 540
QY 541 ATGTCATTAGCTATTTAGATTAACCAAAAAATGGCTAAAGTGTAATACCAAAAGATAC 600
    |||
DB 541 ATGTCATTAGCTATTTAGATTAACCAAAAAATGGCTAAAGTGTAATACCAAAAGATAC 600
QY 601 AACACCTACAGTGAAGATGACGGGTATGATGATGATGATGATGATGATGATGATG 660
    |||
DB 601 AACACCTACAGTGAAGATGACGGGTATGATGATGATGATGATGATGATGATGATG 660
QY 661 CAGTGTAAATTCATTTTACCCTCCGACGATTAATCTAGTGAATGATGATGATGATG 720
    |||
DB 661 CAGTGTAAATTCATTTTACCCTCCGACGATTAATCTAGTGAATGATGATGATGATG 720
QY 721 TAAAGGTGAATTAATTAATGTTTACGGAAGATTAATCAAGATGGGGAGAAAAATCCGA 780
    |||
DB 721 TAAAGGTGAATTAATTAATGTTTACGGAAGATTAATCAAGATGGGGAGAAAAATCCGA 780
QY 781 TTATGACCGCAGAGAGCCAGGTTTCCATGGAATTTAAAAAAGTAAAGATGCAAAAC 840
    |||
DB 781 TTATGACCGCAGAGAGCCAGGTTTCCATGGAATTTAAAAAAGTAAAGATGCAAAAC 840
QY 841 ATATAGTTTACAGATTTTATGATGATGATGATGATGATGATGATGATGATGATGAT 900
    |||
DB 841 ATATAGTTTACAGATTTTATGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 901 TGTTCCTCATGACACTTTGAGAGCGCAAGTTTACTGTTCTGAGAGATGCAATGAGA 960
    |||
DB 901 TGTTCCTCATGACACTTTGAGAGCGCAAGTTTACTGTTCTGAGAGATGCAATGAGA 960
QY 961 GGTATGCGACCACTATATAGAAAAACAGAGAGAGAGATGAGAGATGAGAGAGA 1020
    |||
DB 961 GGTATGCGACCACTATATAGAAAAACAGAGAGAGAGATGAGAGATGAGAGAGA 1020
QY 1021 CGGAAACCTCGAG 1034
    |||
DB 1021 CGGAAACCTCGAG 1034

```

```

RESULT 2
US-09-976-605-7
; Sequence 7, Application US/09976605
; Patent No. US20020102535a1
; GENERAL INFORMATION:
; APPLICANT: MCFADEN, GRANT
; APPLICANT: ESSANI, KARIM
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND POLYPEPTIDES
; FILE REFERENCE: 50082/015002
; CURRENT APPLICATION NUMBER: US/09/976,605
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 60/239,354
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0

```

```

; SEQ ID NO 7
; LENGTH: 1017
; TYPE: DNA
; ORGANISM: Yaba-like disease virus
US-09-976-605-7
Query Match          95.4%; Score 986.6; DB 10; Length 1017;
Best Local Similarity 98.1%; Pred. No. 3,1e-211;
Matches 998; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 8 ATGATATAGTAAATATATTTAGCAAAATTTAGCAAGTTTGTAACTGATTAATAA 67
    |||
DB 1 ATGATATAGTAAATATATTTAGCAAAATTTAGCAAGTTTGTAACTGATTAATAA 60
QY 68 TATATATATCTGTACGTAAAGATTAATGGGTATAGATGATATTTAGCATAT 127
    |||
DB 61 TATATATATCTGTACGTAAAGATTAATGGGTATAGATGATATTTAGCATAT 120
QY 128 TACACGATCAGTTAGTACGAAATATCATATATACCAAGAACTAGACAGGAAACGTA 187
    |||
DB 121 TACACGATCAGTTAGTACGAAATATCATATATATACCAAGAACTAGACAGGAAACGTA 180
QY 188 AATTTAGGCGTATGTTGTTTATATTTCTAGAGATCCCAACGCGAGTAACGATTAC 247
    |||
DB 181 AATTTAGGCGTATGTTGTTTATATTTCTAGAGATCCCAACGCGAGTAACGATTAC 240
QY 248 AACTTTACTTTTGGTATCTTATTAAGAAAGACTTGAAGAAATTAATAAAGCAT 307
    |||
DB 241 AACTTTACTTTTGGTATCTTATTAAGAAAGACTTGAAGAAATTAATAAAGCAT 300
QY 308 AGCAAAAGCTACTTCGCTTCTTATTAACACGCGGTTTGAACAGATTAATATTT 367
    |||
DB 301 AGCAAAAGCTACTTCGCTTCTTATTAACACGCGGTTTGAACAGATTAATATTT 360
QY 368 GGTATGATGGGTATGATGAGAAAGCGCAACGACCGTTGGCCAGATACAGAGAT 427
    |||
DB 361 GGTATGATGGGTATGATGAGAAAGCGCAACGACCGTTGGCCAGATACAGAGAT 420
QY 428 AAAAGGTTTACGAAATGACACATTAAGGTTTCCAGAGTTGGAATGTTAACTGTAAA 487
    |||
DB 421 AAAAGGTTTACGAAATGACACATTAAGGTTTCCAGAGTTGGAATGTTAACTGTAAA 480
QY 488 AACCTCTTTGGAAGATGTAAGAACTTATCTAGGCGGTTTGAATACATGGATGTCA 547
    |||
DB 481 AACCTCTTTGGAAGATGTAAGAACTTATCTAGGCGGTTTGAATACATGGATGTCA 540
QY 548 TTACCTATTTAGATTAACCAAAAAATGCTTAAAGTGAATATCCAAAAGATACACACT 607
    |||
DB 541 TTACCTATTTAGATTAACCAAAAAATGCTTAAAGTGAATATCCAAAAGATACACACT 600
QY 608 ACACTGAAAGTAAAGGTTATGATGATGATGATGATGATGATGATGATGATGATGAT 667
    |||
DB 601 ACACTGAAAGTAAAGGTTATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 668 AATTCATTTTACCCTCCGACGTAATTAATGATGATGATGATGATGATGATGATGAT 727
    |||
DB 661 AATTCATTTTACCCTCCGACGTAATTAATGATGATGATGATGATGATGATGATGAT 720
QY 728 GAATATATATATGTTAAGCGAAGTACTATTCAGAAATGGGGGAGAAAAATCCGATTATG 787
    |||
DB 721 GAATATATATATGTTAAGCGAAGTACTATTCAGAAATGGGGGAGAAAAATCCGATTATG 780
QY 788 CCAGAGAGCGAGGTTTCCATGATGATTAATTAATTAATTAATTAATTAATTAATTAAT 847
    |||
DB 781 CCAGAGAGCGAGGTTTCCATGATGATTAATTAATTAATTAATTAATTAATTAATTAAT 840
QY 848 TTAACAGATTTAGTACGTACCAACATCAAAATAGATGATGATGATGATGATGATGAT 907
    |||
DB 841 TTAACAGATTTAGTACGTACCAACATCAAAATAGATGATGATGATGATGATGATGAT 900
QY 908 CATGACACTTTAGAGCGCAAGTTTATCTGTTCTGAAGATGCAATGAGAGCTATAC 967
    |||
DB 901 CATGACACTTTAGAGCGCAAGTTTATCTGTTCTGAAGATGCAATGAGAGCTATAC 960

```


[illegible]

RESULT 8
US-09-844-653-5/c
; Sequence 5, Application US/09844653

	Query Match	4.1%;	Score 42;	DB 9;	Length 402850;
	Best Local Similarity	51.6%;	Pred. No. 1.1e+02;		
	Matches	96;	Conservative	0;	Mismatches 90;
				Indels	0;
				Gaps	0;
QY	31	CACAAATTGAGCAGTTTGTACTGCATACTTTAAAAATAATATATACCTGTACCTTAA	90		
Db	160962	CATAATAGTGTCCAGTGTCCAAAGAGTCTTTACACCTATATATGATTTGGTTAAGCAAC	160900		
QY	91	AGATATGGGTATTCGATGAGATTTTTCAGATCATTTCAACGATCAGTTAGTACGAA	150		
Db	160902	TGATGCAAGATTCAGAGAGGAGGAGGTTTTCAGCAATATATTTAAATCCTGTGTGCCAA	160843		
QY	151	AATATCATTAACCAAGAACTAGCAACAGGAATAATTTTGGCGTGTGGTTTAA	210		
Db	160842	TTACGCTCTTTAAAGAAAAGACAAAGGGGACCTTATTTTCCTTATATTAATTTAGTTCA	160783		
QY	211	TATTTT	216		
Db	160782	AATCTC	160777		

US-09-864-761-13293
 * Sequence 13293, Application US/09864761A
 * Patent No. US20020048763A1
 * GENERAL INFORMATION
 * APPLICANT: Penn, Sharon G.
 * APPLICANT: Rank, David R.
 * APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 FILE REFERENCE: Aecm1ca-x-1
 CURRENT FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US/09/864,761
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: GB 24263.6
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00663
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00662
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00661
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00670
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 60/234,687
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/774,203
 PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 49117
 SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
 SEQ ID NO 13293
 LENGTH: 563
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AC012404.4
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2
 US-09-864-761-13293

Query Match 4.0%; Score 41.6; DB 10; Length 563;
 Best Local Similarity 51.0%; Pred. No. 7.4;
 Matches 98; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 835 AACACATATAGTTTACGATTTAGTACGTACATCAAAATGAGTCACTAGT 894
 DB 112 AATTAATATATTTTAAATGTAAGATGAAATGTAAGATGTAATTAATTAAT 171
 QY 895 ATGTGTTTTCATGACACTTATAGACGCAAGTTTACTTGTCTGAAGATGCA 954
 DB 172 TCACACGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 231
 QY 955 TGGAGAGCTATACGACCACTATATAGAAACAGAAAGAAAGAAAGTGAAGAGATCA 1014
 DB 232 GGAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 291
 QY 1015 AGAAGACGCAAA 1026

DB 292 AGAAGAAAGAAAGAA 303
 RESULT 10
 US-09-938-842A-3532
 Sequence 3532, Application US/09938842A
 Patent No. US20020160378A1
 GENERAL INFORMATION:
 APPLICANT: Harper, Jeff
 APPLICANT: Krepis, Joel
 APPLICANT: Wang, Xun
 APPLICANT: Zhu, Tong
 TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 FILE REFERENCE: SCRIPI300-3
 CURRENT APPLICATION NUMBER: US/09/938,842A
 PRIOR FILING DATE: 2001-08-24
 PRIOR APPLICATION NUMBER: US 60/227,866
 PRIOR FILING DATE: 2000-08-24
 PRIOR APPLICATION NUMBER: US 60/264,647
 PRIOR FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: US 60/300,111
 PRIOR FILING DATE: 2001-06-22
 NUMBER OF SEQ ID NOS: 5379
 SEQ ID NO 3532
 LENGTH: 2000
 TYPE: DNA
 ORGANISM: Arabidopsis thaliana
 US-09-938-842A-3532

Query Match 4.0%; Score 41; DB 9; Length 2000;
 Best Local Similarity 45.7%; Pred. No. 18;
 Matches 143; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 55 CATACCTTAAATATATATATATATCTGTACGTAAAGAAATGCGTTATACATGAGT 114
 DB 362 CATAGAAATGAAACAAATGATATGTAATGTAACCAAAAGGTGAACATATATTA 421
 QY 115 ATTATACATATACATACATGATGATGATGATGATGATGATGATGATGATGATG 174
 DB 422 ACATTAAGATATACATTAATTAATGATGATGATGATGATGATGATGATGATG 481
 QY 175 ACACGGAAGCTAATATTTAGGCGTGAATGATGATGATGATGATGATGATGATG 234
 DB 482 AAGTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 541
 QY 235 AGTAAAGATATACATCTTACCTTGTGATGATGATGATGATGATGATGATGATG 294
 DB 542 ATTTATATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 601
 QY 295 TAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 354
 DB 602 TTATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 661
 QY 355 AGATTTATATTT 367
 DB 662 AGTATATATATAT 674

RESULT 11
 US-10-239-676-190/c
 Sequence 190, Application US/10239676
 Publication No. US20030082609A1
 GENERAL INFORMATION:
 APPLICANT: OLEK, Alexander
 APPLICANT: PIPENBROCK, Christian
 APPLICANT: BERLIN, Kurt
 TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
 FILE REFERENCE: 5013.1003
 CURRENT APPLICATION NUMBER: US/10/239,676
 CURRENT FILING DATE: 2002-09-24
 PRIOR APPLICATION NUMBER: PCT/EP01/03968

DE 10019058.8
DE 10019173.8
DE 10032529.7
DE 10043826.1
PRIOR FILING DATE: 2001-04-06
2000-04-06
2000-04-07
2000-06-30
2000-09-01
NUMBER OF SEQ ID NOS: 228
SEQ ID NO 190
LENGTH: 6204
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-09-754-853A-2

Query Match 3.9%; Score 40.2; DB 9; Length 6204;
Best Local Similarity 50.8%; Pred. No. 44;
Matches 96; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 428 AAAGGTTACGAAATGACATATAGGTTTCCCAAGTTGGATGTTAACTGTAATA 487
DB 2352 AAAACATATATTAATTCATTAATAAATAATATATCAAAATTAACATTAATAA 2293
QY 488 AACACTTTTGAAAGATGTAATACTATCTAGCGGTTTGAATCATGGATGTTCA 547
DB 2292 TAAATCCTTTTAAATTTTATCTTAACTATTCGATTAACCAACAAATATTTAA 2233
QY 548 TTACGATTTTATGATTAACCAAAATGCTTAAGTGAAATACCAAAAGATACACCT 607
DB 2232 TAAATATATTTTAAACCAACCAAAATTAATAAACCTTAATATATCAACAT 2173
QY 608 ACAGTGA 616
DB 2172 ACACAAAA 2164

RESULT 12

US-09-754-853A-2/c
; Sequence 2, Application US/09754853A
; Publication No. US20030005491A1
; GENERAL INFORMATION:
; APPLICANT: Hauge, Brian M.
; APPLICANT: Parnell, Laurence D.
; APPLICANT: Parsons, Jeremy D.
; APPLICANT: Wang, Ming Li
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-10(15810)B
; CURRENT APPLICATION NUMBER: US/09/754,853A
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,880
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 1119
; SEQ ID NO 2
; LENGTH: 335913
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (45163)..(45314)..(45450)..(45509)..(46941)..(48763)..(48975)..(49573)
; OTHER INFORMATION: Clone ID: 240017_region_G3
US-09-754-853A-2

Query Match 3.9%; Score 40; DB 9; Length 335913;
Best Local Similarity 45.5%; Pred. No. 2.7e+02;

Matches 142; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 5 TTCAATGATTAATTAATTTAGCAATGTTAGCGTTTGAATGATTAATTTAA 64
DB 280510 TTTTATATTAATTAATTTAGCAATGTTAGCGTTTGAATGATTAATTTAA 280451

QY 65 AAATATATTAATTAATTTAGCAATGTTAGCGTTTGAATGATTAATTTAA 124
DB 280450 AAATATATTAATTAATTTAGCAATGTTAGCGTTTGAATGATTAATTTAA 280391
QY 125 CATTAACAGATGATTAATTAATTTAGCAATGTTAGCGTTTGAATGATTAATTTAA 184
DB 280390 AAATATATTAATTAATTTAGCAATGTTAGCGTTTGAATGATTAATTTAA 280331
QY 185 GTAAATTTAGGCGTATGTTATTAATTTAGCAATGTTAGCGTTTGAATGATTAATTTAA 244
DB 280330 ATGAGATTTTATTAATTTAGCAATGTTAGCGTTTGAATGATTAATTTAA 280271
QY 245 TACAACTTTAGGCGTATGTTATTAATTTAGCAATGTTAGCGTTTGAATGATTAATTTAA 304
DB 280270 AAATATATTAATTTAGCAATGTTAGCGTTTGAATGATTAATTTAA 280211
QY 305 GATAGCAAAAA 316
DB 280210 TATTAATTTAA 280199

RESULT 13

US-09-754-853A-3/c
; Sequence 3, Application US/09754853A
; Publication No. US20030005491A1
; GENERAL INFORMATION:
; APPLICANT: Hauge, Brian M.
; APPLICANT: Parnell, Laurence D.
; APPLICANT: Parsons, Jeremy D.
; APPLICANT: Wang, Ming Li
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-10(15810)B
; CURRENT APPLICATION NUMBER: US/09/754,853A
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,880
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 1119
; SEQ ID NO 3
; LENGTH: 335913
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (46798)..(48763)..(48975)..(49573)
; OTHER INFORMATION: Clone ID: 240017_region_G3
US-09-754-853A-3

Query Match 3.9%; Score 40; DB 9; Length 335913;
Best Local Similarity 45.5%; Pred. No. 2.7e+02;

Matches 142; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 5 TTCAATGATTAATTAATTTAGCAATGTTAGCGTTTGAATGATTAATTTAA 64
DB 280510 TTTTATATTAATTAATTTAGCAATGTTAGCGTTTGAATGATTAATTTAA 280451
QY 65 AAATATATTAATTAATTTAGCAATGTTAGCGTTTGAATGATTAATTTAA 124
DB 280450 AAATATATTAATTAATTTAGCAATGTTAGCGTTTGAATGATTAATTTAA 280391
QY 125 CATTAACAGATGATTAATTAATTTAGCAATGTTAGCGTTTGAATGATTAATTTAA 184
DB 280390 AAATATATTAATTAATTTAGCAATGTTAGCGTTTGAATGATTAATTTAA 280331
QY 185 GTAAATTTAGGCGTATGTTATTAATTTAGCAATGTTAGCGTTTGAATGATTAATTTAA 244
DB 280330 ATGAGATTTTATTAATTTAGCAATGTTAGCGTTTGAATGATTAATTTAA 280271
QY 245 TACAACTTTAGGCGTATGTTATTAATTTAGCAATGTTAGCGTTTGAATGATTAATTTAA 304
DB 280270 AAATATATTAATTTAGCAATGTTAGCGTTTGAATGATTAATTTAA 280211

QY 305 GATGACACAAA 316
 DB 280210 TATTAATTTAA 280199

RESULT 14

US-09-790-988-1
 ; Sequence 1, Application US/09790988
 ; Patent No. US20020127687A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SHIGENOBU, SHUJI
 ; APPLICANT: WATANABE, HIDEMI
 ; APPLICANT: HATORI, MASAHIRA
 ; APPLICANT: SAKAKI, YOSHIYUKI
 ; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
 ; FILE REFERENCE: 081356/0159
 ; CURRENT APPLICATION NUMBER: US/09/790,988
 ; PRIOR FILING DATE: 2001-02-23
 ; PRIOR APPLICATION NUMBER: JP2000-107160
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 640681
 ; TYPE: DNA
 ; ORGANISM: Buchnera sp.
 US-09-790-988-1

Query Match 3.8%; Score 39.8; DB 10; Length 640681;
 Best Local Similarity 52.8%; Pred. No. 3.7e+02;
 Matches 86; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 56 ATAACTTTAAATATATATCTGTTAGCTTAAAGATAAGGTTATACGATGAGTA 115
 DB 527243 ATATCTTTAAATTTTATTTTATATACATTAATGATATCATTTTGACATGATATA 527302
 QY 116 TTTTACGATCATACAGTCATGATGATACGAAATATCATATACCAAGAACTAGA 175
 DB 527303 ATCAAAATGTTATCAAAAAATTTTATGATCAAAAAACAAATTTTATCTTAA 527362
 QY 176 CACGAAACGTAATTTTAGGCGCTGATGTTATATTTCTA 218
 DB 527363 AATTAACACTTTATTTGTTAAAAACCCCTTTTATATATCTA 527405

RESULT 15

US-09-790-988-1/c
 ; Sequence 1, Application US/09790988
 ; Patent No. US20020127687A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SHIGENOBU, SHUJI
 ; APPLICANT: WATANABE, HIDEMI
 ; APPLICANT: HATORI, MASAHIRA
 ; APPLICANT: SAKAKI, YOSHIYUKI
 ; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
 ; FILE REFERENCE: 081356/0159
 ; CURRENT APPLICATION NUMBER: US/09/790,988
 ; CURRENT FILING DATE: 2001-02-23
 ; PRIOR APPLICATION NUMBER: JP2000-107160
 ; PRIOR FILING DATE: 2000-04-07
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 640681
 ; TYPE: DNA
 ; ORGANISM: Buchnera sp.
 US-09-790-988-1

Query Match 3.8%; Score 39.6; DB 10; Length 640681;
 Best Local Similarity 43.5%; Pred. No. 4.1e+02;
 Matches 180; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

QY 498 GGAAGATGTAAACTTATCTAGCGGCTTTTGATATACGAGATGTTCACTTATTT 557

DB 347364 GAAAAACCTTACAGATTCACAACTGAAATTTGCAATTTAAGCATATAGCTTATCAAT 347305
 QY 558 TAGATTACCAAAAAATGGCTAAAGTGAAATACCAAAAGATACACACTTACAGTGAAG 617
 DB 347304 TATTTAAAGAAACAAAAATATTTAAGATTAATAAATGAAATGTTAGACATCAAGCTTTAC 347245
 QY 618 TAACGGTAATGATGTAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 677
 DB 347244 AGTCAAGTAAAGATTTTAAAGCTTCTAAATTTGAATTTATCTTTTAAAGAAAAATAC 347185
 QY 678 ACCCTGCTGACGTAATTTACTAAGTGAAGAGCAATTTTAAAGGTGAATTAAT 737
 DB 347184 ATCATTTTCTATGTCATGATACCTAATTTCTCTGACGATGTCAGAGGAAATACAT 347125
 QY 738 ATGTAAAGGAAGATACATACAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 797
 DB 347124 CGATTAAATTAATTAAGAAATTTAAATCTGGGCTCAAAAAAGAGATATGATTTGAAATCC 347065
 QY 798 CAGTTTTCATGCAATTAATTTAAAAAGATTAAGATCAACATATAGTTTACAGATT 857
 DB 347064 AAGATCATATAGAGCTAGGAAAAATTTTAAAGATTTAGATTGGAATCTTCTGACAAA 347005
 QY 858 TAGTACGTACACATCAAAATGAGTACATCACTAGTATGTTGTTTCCATG 911
 DB 347004 TGTCAAGATCAGATTTGTTATTAATGAAGGAAAAATTTCTTTTACACCGTG 346951

Search completed: June 15, 2003, 21:41:34
 Job time : 194 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 19:36:31 ; Search time 2746 Seconds

(without alignments)
10958.595 Million cell updates/sec

Title: US-09-976-605-5

Perfect score: 1034
Sequence: 1 aagctcatgataaagtaaa.....agaagacgaacccctcgag 1034

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBankl:*

1: gb_da:*

2: gb_hcg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_da:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_hcg_hum:*

31: em_hcg_inv:*

32: em_hcg_other:*

33: em_hcg_mus:*

34: em_hcg_pln:*

35: em_hcg_rod:*

36: em_hcg_mam:*

37: em_hcg_vrt:*

38: em_sy:*

39: em_hcgo_hum:*

40: em_hcgo_mus:*

41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	991.6	95.9	144575	14	YD1293568	AJ293568 Yaba-like
2	133.6	12.9	1023	6	AR145601	AR145601 Sequence
3	133.6	12.9	1023	6	IS8315	IS8315 Sequence 53
4	133.6	12.9	1023	6	IS8315	L21931 Swinepox v1
5	133.6	12.9	14176	6	AR145576	AR145576 Sequence
6	133.6	12.9	14176	6	AR145583	AR145583 Sequence
7	133.6	12.9	14176	6	IS8290	IS8290 Sequence 1
8	133.6	12.9	14176	6	IS8297	IS8297 Sequence 14
9	133.6	12.9	14176	14	SMFHL5B	L22013 Swinepox v1
10	133.6	12.9	146454	14	AF410153	AF410153 Swinepox
11	133.6	12.9	146454	14	AF410153	AF410153 Swinepox
12	133.6	12.9	146454	14	AF410153	AF410153 Swinepox
13	58.6	5.7	5420	3	AF056936	AF056936 Plasmid
14	57.2	5.5	133501	2	AC116956	AC116956 Dictyoste
15	57.2	5.5	4102	3	AF270648	AF270648 Plasmid
16	56.8	5.5	216508	10	AL683805	AL683805 Mouse DNA
17	55.4	5.4	1141	6	AX083744	AX083744 Sequence
18	54.8	5.3	914	6	PFRESA	X55124 P. falcipar
19	53.4	5.2	1141	6	AX083744	AX083744 Sequence
20	51.6	5.0	112698	2	AC119418	AC119418 Medicago
21	51.6	5.0	129096	2	AC126019	AC126019 Medicago
22	51.2	5.0	293431	2	PFMAL13P4	AL049181 Plasmid
23	51.2	4.9	6306	6	AX281184	AX281184 Sequence
24	51.2	4.9	6306	6	AX281184	AX281184 Sequence
25	50.4	4.9	146383	2	AC116330	AC116330 Dictyoste
26	50.2	4.9	82469	2	AF206632	AF206632 Plasmid
27	50.2	4.8	825	2	AF206632	AF206632 Plasmid
28	49.8	4.8	185558	2	AC129389	AC129389 Rattus no
29	49.4	4.8	1686	6	E08895	E08895 DNA encodin
30	49.4	4.8	135559	8	CPU030821	U30821 Cyanophora
31	49.4	4.8	192581	2	PFMAL13P1	AL049180 Plasmid
32	49.4	4.7	6175	6	AX346209	AX346209 Sequence
33	49.4	4.7	178098	2	AC040955	AC040955 Mus muscu
34	48.8	4.7	4995	3	PFAMESA	M69183 Plasmid
35	48.8	4.7	60182	2	PFMAL1P6	AL031749 Plasmid
36	48.6	4.7	175159	2	AC097877	AC097877 Rattus no
37	48.6	4.7	182025	9	AL138900	AL138900 Human DNA
38	47.8	4.6	1055	6	AX083745	AX083745 Sequence
39	47.8	4.6	29016	2	AC117266	AC117266 Dictyoste
40	47.6	4.6	1324	3	PFRESA1	X05182 P. falcipar
41	47.6	4.6	4591	6	A00661	A00661 P. falcipar
42	47.6	4.6	245802	2	AC006279	AC006279 Plasmid
43	47.6	4.6	34980	6	AX344559	AX344559 Sequence
44	47.4	4.6	158094	2	AC108623	AC108623 Rattus no
45	47.4	4.6	158255	2	AC112577	AC112577 Rattus no

ALIGNMENTS

Result No.	Score	Query Match	Length	DB	ID	Description
1	991.6	95.9	144575	14	YD1293568	AJ293568 Yaba-like
2	133.6	12.9	1023	6	AR145601	AR145601 Sequence
3	133.6	12.9	1023	6	IS8315	IS8315 Sequence 53
4	133.6	12.9	1023	6	IS8315	L21931 Swinepox v1
5	133.6	12.9	14176	6	AR145576	AR145576 Sequence
6	133.6	12.9	14176	6	AR145583	AR145583 Sequence
7	133.6	12.9	14176	6	IS8290	IS8290 Sequence 1
8	133.6	12.9	14176	6	IS8297	IS8297 Sequence 14
9	133.6	12.9	14176	14	SMFHL5B	L22013 Swinepox v1
10	133.6	12.9	146454	14	AF410153	AF410153 Swinepox
11	133.6	12.9	146454	14	AF410153	AF410153 Swinepox
12	133.6	12.9	146454	14	AF410153	AF410153 Swinepox
13	58.6	5.7	5420	3	AF056936	AF056936 Plasmid
14	57.2	5.5	133501	2	AC116956	AC116956 Dictyoste
15	57.2	5.5	4102	3	AF270648	AF270648 Plasmid
16	56.8	5.5	216508	10	AL683805	AL683805 Mouse DNA
17	55.4	5.4	1141	6	AX083744	AX083744 Sequence
18	54.8	5.3	914	6	PFRESA	X55124 P. falcipar
19	53.4	5.2	1141	6	AX083744	AX083744 Sequence
20	51.6	5.0	112698	2	AC119418	AC119418 Medicago
21	51.6	5.0	129096	2	AC126019	AC126019 Medicago
22	51.2	5.0	293431	2	PFMAL13P4	AL049181 Plasmid
23	51.2	4.9	6306	6	AX281184	AX281184 Sequence
24	51.2	4.9	6306	6	AX281184	AX281184 Sequence
25	50.4	4.9	146383	2	AC116330	AC116330 Dictyoste
26	50.2	4.9	82469	2	AF206632	AF206632 Plasmid
27	50.2	4.8	825	2	AF206632	AF206632 Plasmid
28	49.8	4.8	185558	2	AC129389	AC129389 Rattus no
29	49.4	4.8	1686	6	E08895	E08895 DNA encodin
30	49.4	4.8	135559	8	CPU030821	U30821 Cyanophora
31	49.4	4.8	192581	2	PFMAL13P1	AL049180 Plasmid
32	49.4	4.7	6175	6	AX346209	AX346209 Sequence
33	49.4	4.7	178098	2	AC040955	AC040955 Mus muscu
34	48.8	4.7	4995	3	PFAMESA	M69183 Plasmid
35	48.8	4.7	60182	2	PFMAL1P6	AL031749 Plasmid
36	48.6	4.7	175159	2	AC097877	AC097877 Rattus no
37	48.6	4.7	182025	9	AL138900	AL138900 Human DNA
38	47.8	4.6	1055	6	AX083745	AX083745 Sequence
39	47.8	4.6	29016	2	AC117266	AC117266 Dictyoste
40	47.6	4.6	1324	3	PFRESA1	X05182 P. falcipar
41	47.6	4.6	4591	6	A00661	A00661 P. falcipar
42	47.6	4.6	245802	2	AC006279	AC006279 Plasmid
43	47.6	4.6	34980	6	AX344559	AX344559 Sequence
44	47.4	4.6	158094	2	AC108623	AC108623 Rattus no
45	47.4	4.6	158255	2	AC112577	AC112577 Rattus no

14L gene; 15OR gene; 15IR gene; 15L gene; 16L gene; 17L gene; 18L gene; 19L gene; 1L gene; 20L gene; 21L gene; 22L gene; 23L gene; 24L gene; 25L gene; 26L gene; 27L gene; 28R gene; 29L gene; 2L gene; 3-Beta-hydroxysteroid dehydrogenase; 30L gene; 31R gene; 32L gene; 33L gene; 34L gene; 35L gene; 36R gene; 37R gene; 38R gene; 39L gene; 3L gene; 40R gene; 41L gene; 42L gene; 43L gene; 44L gene; 45L gene; 46L gene; 47L gene; 48L gene; 49R gene; 4L gene; 50L gene; 51L gene; 52R gene; 53L gene; 54R gene; 55R gene; 56R gene; 57L gene; 58R gene; 59R gene; 5L gene; 60R gene; 61R gene; 62L gene; 63R gene; 64R gene; 65R gene; 66R gene; 67R gene; 68R gene; 69R gene; 6L gene; 70L gene; 71R gene; 72L gene; 73R gene; 74L gene; 75L gene; 76R gene; 77R gene; 78R gene; 79R gene; 7L gene; 80L gene; 81R gene; 82R gene; 83R gene; 84R gene; 85R gene; 86R gene; 87R gene; 88L gene; 89L gene; 8L gene; 90L gene; 91L gene; 98L gene; 99R gene; 9L gene; 94L gene; 95L gene; 96R gene; 97L gene; 98L gene; 99R gene; 9L gene; CC chemokine receptor; CD46-like proteinase; CD47-like protein; DNA helicase; DNA polymerase; DNA polymerase processivity factor; DNA topoisomerase II; DNA-binding protein; DNA/RNA-binding protein/virio; dsRNA-binding virion core dtrpase; early transcription factor; eIF2-alpha mimic and anti-interfero; extracellular virus membran; extracellular virus membran protein; glutaredoxin 2; host range protein; Interleukin alpha/beta receptor; Interleukin-18 binding protein; Interferon gene transcription facto; late transcription elongation factor; late transcription factor2; late transcription elongation factor; late gene transcription factor; mda-7-like or interleukin-10-like; membrane-associated viron protein; monoglyceride lipase; mRNA capping enzyme large subunit; mRNA capping enzyme small subunit; Mult protein; myristylprotein; negative regulator of gene expression; nucleoside triphosphat; poly(A) polymerase catalytic subunit; poly(A) polymerase regulatory subunit; protease; ribonucleotide reductase small subunit; RNA and DNA helicase; RNA polymerase associated transcripto; RNA polymerase elongation factor; RNA polymerase subunit rp0132; RNA polymerase subunit rp0147; RNA polymerase subunit rp018; RNA polymerase subunit rp019; RNA polymerase subunit rp022; RNA polymerase subunit rp030; RNA polymerase subunit rp035; RNA polymerase subunit rp07; role in virus DNA packaging; secreted OX-2-like protein; secreted protein; serine protease; serine protease inhibitor; serine/threonine protein kinase; soluble MHC-I-like protein; ssDNA-binding myristylprotein; transmembrane protein; tyrosine/serine phosphatase; uracil DNA glycosylase; viron core structural protein p4a; viron membrane protein; viron protein; viron structural core protein; viron structural protein; viron surface protein; yaba-like disease virus.

Yaba-like disease virus.

Yabnses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae; Yatapoxvirus.

1 (bases 1 to 144575)

Lee, H. J.

Thesis (2000) Sir William Dunn School of Pathology, University of Oxford, Oxford, UNITED KINGDOM

2 (bases 1 to 144575)

Lee, H. J., Essani, K. and Smith, G. L.

The genome sequence of yaba-like disease virus, a yatapoxvirus

JOURNAL Virology 281 (2), 170-192 (2001)

21176366

PUBMED 11277691

3 (bases 1 to 144575)

Lee, H. J.

Direct Submission

Submitted (13-JUL-2000) Lee H. J., Sir William Dunn School of Pathology, University of Oxford, South Parks road, Oxford, OX1 3RE, UNITED KINGDOM

1. 144575

location/Qualifiers

FEATURES

SOURCE

```
Location/Qualifiers
1. .144575
/organism="Yaba-like disease virus"
/virion
/db_xref="taxon:132475"
complement(755. .1756)
```

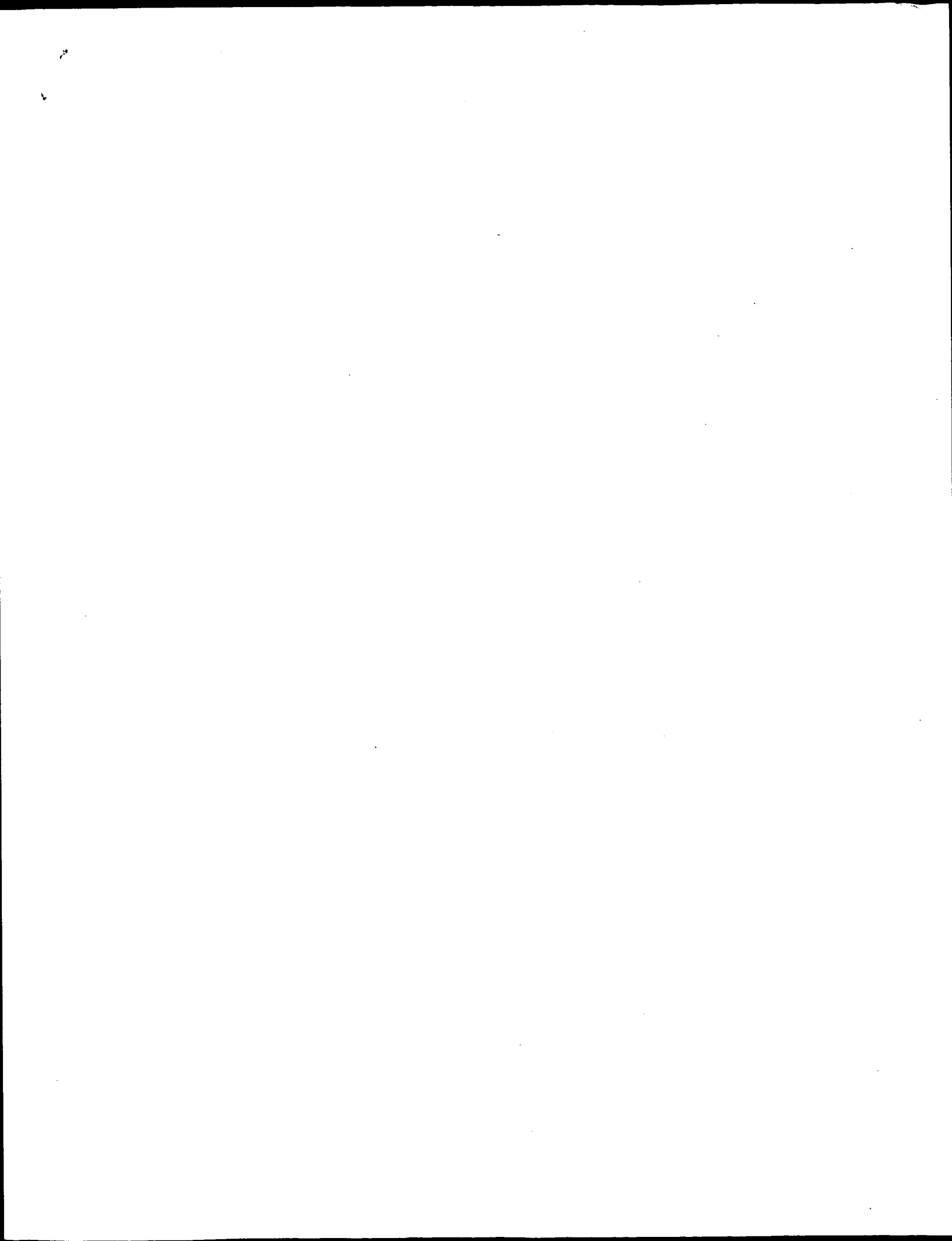
gene sig_peptide

CDS
complement(755. .1756)
/gene="1L"
/function-"Unknown"
/citation-[2]
/codon_start=1
/product="1L protein"
/protein_id="CAC21239.1"
/db_xref="GI:12056160"
/db_xref="SPRMBL:O9DHV2"
/translation-"MEYITDGVLTAKLSFRDFRGIKKEELFNALSWEDSDILNRHROF
PCELVLLEKSEERTKYVGAVKRVLASLSLDNYVCHEHLIVCFPGVGPDNFSII
EDNRGSEVEYLVAHLSSPKNGKTDCVCGDVGYIATADPELKERESGLANVQREBE
ILVALVFYFLRKADVLFETLARSKDYCFEYERGDGNLCYALVEVNSPRAPYSREV
TDSGRKLVDNRQYOKLVKRYAKVTDMOTESTPFGFNLSWEKDKAMRELKRV
EDLMVSRSEDDEYFKLTVLYVYSNMKTAVDYVLTSTCDDEDIQYISLVNIKCYFSI
complement(1869. .2885)
/gene="2L"
complement(1869. .2885)
/gene="2L"
/function-"putative soluble MHC-I-like protein"
/note-"related to swinepox virus C1L and chicken MHC-I"
/citation-[2]
/codon_start=1
/product="2L protein"
/protein_id="CAC21240.1"
/db_xref="GI:12056161"
/db_xref="SPRMBL:O9DHW0"
/translation-"MDKLIFSLIYACNCITLKKNYVTLNDGLTDGVFYDHYND
LVAKISYNETHRGHGNFPAIDWFNTSRSPHTGNDGNYNRFMISLKEKTEINKNDS
KITTSILINGCYETGLIGSGSYCEYEPANGPLARKITDGKRFVKMHKGPPKMGMLTV
NLIMDDVKRYAIGGPETMGCSLAILDTQRKAQKIRKDTPTPVKYGNELEDGNMTLEK
YNSRPFPVYITKWLEISEKFKEYVNGRRYPENGRKSNTPEGGPFPMNIKDKDKD
NTISLDLTRTYSKMSQPCVCFHDITLAQYTCSECNGELVHLTRKIEEGGE
DED"

sig_peptide

gene
complement(2838. .2885)
/gene="2L"
/citation-[2]
complement(2932. .3600)
/gene="3L"
complement(2932. .3600)
/gene="3L"
/function-"Unknown"
/note-"related to swinepox virus CSL and vaccinia virus strain Copenhagen K7R"
/citation-[2]
/codon_start=1
/product="3L protein"
/protein_id="CAC21241.1"
/db_xref="GI:12056162"
/db_xref="SPRMBL:O9DHV9"
/translation-"MEEKIMEKIXILKSKREPQSFISFWNADFAFYDQRLNEL
LKIRLEEYGGNVRLIIDYISIVSTCKMKTKDENNDLLITSNLANKLFIKKNFYE
KNNSIDDIITYFTWKNNNTVSCGVAFKEIMKXDELAKOYGEKLKDINNFLNK
YKIMTFEFNDPDLNYCKVSIGFVISLDFVEPLYNEDTDFPNQVRSIRYMILLKEELI
STIN"

gene
complement(3630. .4346)
/gene="4L"
complement(3630. .4346)
/gene="4L"
/function-"Unknown"
/note-"related to swinepox virus CSL and vaccinia virus strain Copenhagen NZL"
/citation-[2]
/codon_start=1
/product="4L protein"
/protein_id="CAC21242.1"
/db_xref="GI:12056163"
/db_xref="SPRMBL:O9DHV8"
/translation-"MDYKSLITRYKCICYSNNKNFVEEKKNFVSDDPIDPDEI
VGFLPECPCTYYTIOLISKSNLNKOEVLETSELKCONYVENIFTTTIDHBHLYD
SMASVENFNLMKEYESFPONKNNNNIKIPRELMASTDGLAINHGQLYIKNAIE
INSPRDYSISYIKRRKRKIDDTISVINIDPIKTIIGFISILSVHDYVDNSNISYIFE



gene
complement(4386.4856)
/gene="5L"
complement(4386.4856)
/gene="5L"
/function="Unknown"
/note="related to swinepox virus C7L"
/citation=[2]
/codon_start=1
/product="5L protein"
/protein_id="CAC21243.1"
/db_xref="GI:12056164"
/db_xref="SPRMBL:Q9DHY7"
/translation="MSDLCNDVCEERNNCGCNEEYVIAIKCQMLNYSKKE
CNLCRYNINIKTYVSEKRMWCEKDKTLEKIFLIFLAVYIFLITLSDMANV
TGINDLCSIFLIVYVWLISICFVFAVIVDFLEKAKNSFLTIREY"
complement(4920.5369)
/gene="6L"
complement(4920.5369)
/gene="6L"
/function="Unknown"
/note="related to vaccinia virus strain Copenhagen B15R"
/citation=[2]
/codon_start=1
/product="6L protein"
/protein_id="CAC21244.1"
/db_xref="GI:12056165"
/db_xref="SPRMBL:Q9DHY6"
/translation="MECPGCLVDCINRDDIROLIVDIYYSMSYRSRPAKYF
QVLEFRDSEIVGENRHVYKFKTIGEDYVQAKCTIKNALREVSNADICA
SLAEYWGEDIPTDSIOALIKMIIISDDYSTIDLCNVRILKLA"
complement(5433.6488)
/gene="7L"
complement(5433.6488)
/gene="7L"
/function="putative CC chemokine receptor"
/note="related to Macaca mulatta chemokine receptor and
human CC chemokine receptor type 8"
/citation=[2]
/codon_start=1
/product="7L protein"

Query Match
Best Local Similarity 95.9%; Score 991.6; DB 14; Length 144575;
Matches 1003; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

gene
complement(4386.4856)
/gene="5L"
complement(4386.4856)
/gene="5L"
/function="Unknown"
/note="related to swinepox virus C7L"
/citation=[2]
/codon_start=1
/product="5L protein"
/protein_id="CAC21243.1"
/db_xref="GI:12056164"
/db_xref="SPRMBL:Q9DHY7"
/translation="MSDLCNDVCEERNNCGCNEEYVIAIKCQMLNYSKKE
CNLCRYNINIKTYVSEKRMWCEKDKTLEKIFLIFLAVYIFLITLSDMANV
TGINDLCSIFLIVYVWLISICFVFAVIVDFLEKAKNSFLTIREY"
complement(4920.5369)
/gene="6L"
complement(4920.5369)
/gene="6L"
/function="Unknown"
/note="related to vaccinia virus strain Copenhagen B15R"
/citation=[2]
/codon_start=1
/product="6L protein"
/protein_id="CAC21244.1"
/db_xref="GI:12056165"
/db_xref="SPRMBL:Q9DHY6"
/translation="MECPGCLVDCINRDDIROLIVDIYYSMSYRSRPAKYF
QVLEFRDSEIVGENRHVYKFKTIGEDYVQAKCTIKNALREVSNADICA
SLAEYWGEDIPTDSIOALIKMIIISDDYSTIDLCNVRILKLA"
complement(5433.6488)
/gene="7L"
complement(5433.6488)
/gene="7L"
/function="putative CC chemokine receptor"
/note="related to Macaca mulatta chemokine receptor and
human CC chemokine receptor type 8"
/citation=[2]
/codon_start=1
/product="7L protein"

427 TAAAGGTTACGAAATGACATAGAGTTTCCCAAGTTGAAATGTTAACTGTA 486
|||||
2466 TAAAGGTTACGAAATGACATAGAGTTTCCCAAGTTGAAATGTTAACTGTA 2407
|||||
487 AAACACTTTGGAAAGATGTAAGAACTTATAGCGGGTTTGAATACATGGATGTC 546
|||||
2406 AAACACTTTGGAAAGATGTAAGAACTTATAGCGGGTTTGAATACATGGATGTC 2347
|||||
547 ATTAGCTATTGTAATGTTACCAAAAATGCGTAAAGGTGAATACCAAAAGATCAACACC 606
|||||
2346 ATTAGCTATTGTAATGTTACCAAAAATGCGTAAAGGTGAATACCAAAAGATCAACACC 2287
|||||
607 TACAGTGAAGTAAAGGTTAATGATGTAAGAAATGTTAATGATGTTGATGTTGATGTT 666
|||||
2286 TACAGTGAAGTAAAGGTTAATGATGTAAGAAATGTTAATGATGTTGATGTTGATGTT 2227
|||||
667 AAATGATTTTACCTCTGACGTAATTTACTAGTGAATGAAAGGAAATTTTAAAG 726
|||||
2226 AAATGATTTTACCTCTGACGTAATTTACTAGTGAATGAAAGGAAATTTTAAAG 2167
|||||
727 TGAATTTAAATGTTAAGGAAATGATGATCCAGATGGGGAGAAATCCGATTATGA 786
|||||
2166 TGAATTTAAATGTTAAGGAAATGATGATCCAGATGGGGAGAAATCCGATTATGA 2107
|||||
787 GCGAGAGAGCGAGGTTTCCATGGAATTTAAAGATGCAACACATATAG 846
|||||
2106 GCGAGAGAGCGAGGTTTCCATGGAATTTAAAGATGCAACACATATAG 2047
|||||
847 TTTAAGATTTAGTACGTAACATCAAAATGATGATGATGATGATGATGATGATGAT 906
|||||
2046 TTTAAGATTTAGTACGTAACATCAAAATGATGATGATGATGATGATGATGATGAT 1987
|||||
907 CCATGACATTTGAAGCGCAAGTTTAACTGTTCTGAGAGTCAATGAGAGCTATA 966
|||||
1986 CCATGACATTTGAAGCGCAAGTTTAACTGTTCTGAGAGTCAATGAGAGCTATA 1927
|||||
967 CGACACATTTAGTAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1026
|||||
1926 CGATCACCTTTAGTAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1867
|||||
1027 CC 1028
1866 CC 1865

RESULT 2
ARI45601
LOCUS ARI45601 1023 bp DNA linear PAT 08-NOV-2001
DEFINITION Sequence 53 from patent US 6217882.
ACCESSION ARI45601
VERSION ARI45601.1 GI:15108790
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1023)
AUTHORS Moyer, R.W., Vinuela, E. and Gibbs, E.P.J.
TITLE Use of recombinant swine poxvirus as a live vaccine vector
JOURNAL Patent: US 6217882-A 53 17-Apr-2001;
FEATURES
source location/Qualifiers
BASE COUNT 359 a 158 c 199 g 307 t
ORIGIN

Query Match
Best Local Similarity 12.9%; Score 133.6; DB 6; Length 1023;
Matches 451; Conservative 0; Mismatches 454; Indels 15; Gaps 3;

427 TTAAGCAATGTAAGCAATGTAAGCAATGTAAGCAATGTAAGCAATGTAAGCAATGTAAG 86
|||||
35 TTAAGCAATGTAAGCAATGTAAGCAATGTAAGCAATGTAAGCAATGTAAGCAATGTAAG 94
|||||



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 96300

TO: Ulrike Winkler
Location: cm-1/8d09/8e12
Art Unit: 1648
Monday, June 16, 2003

Case Serial Number: 976605

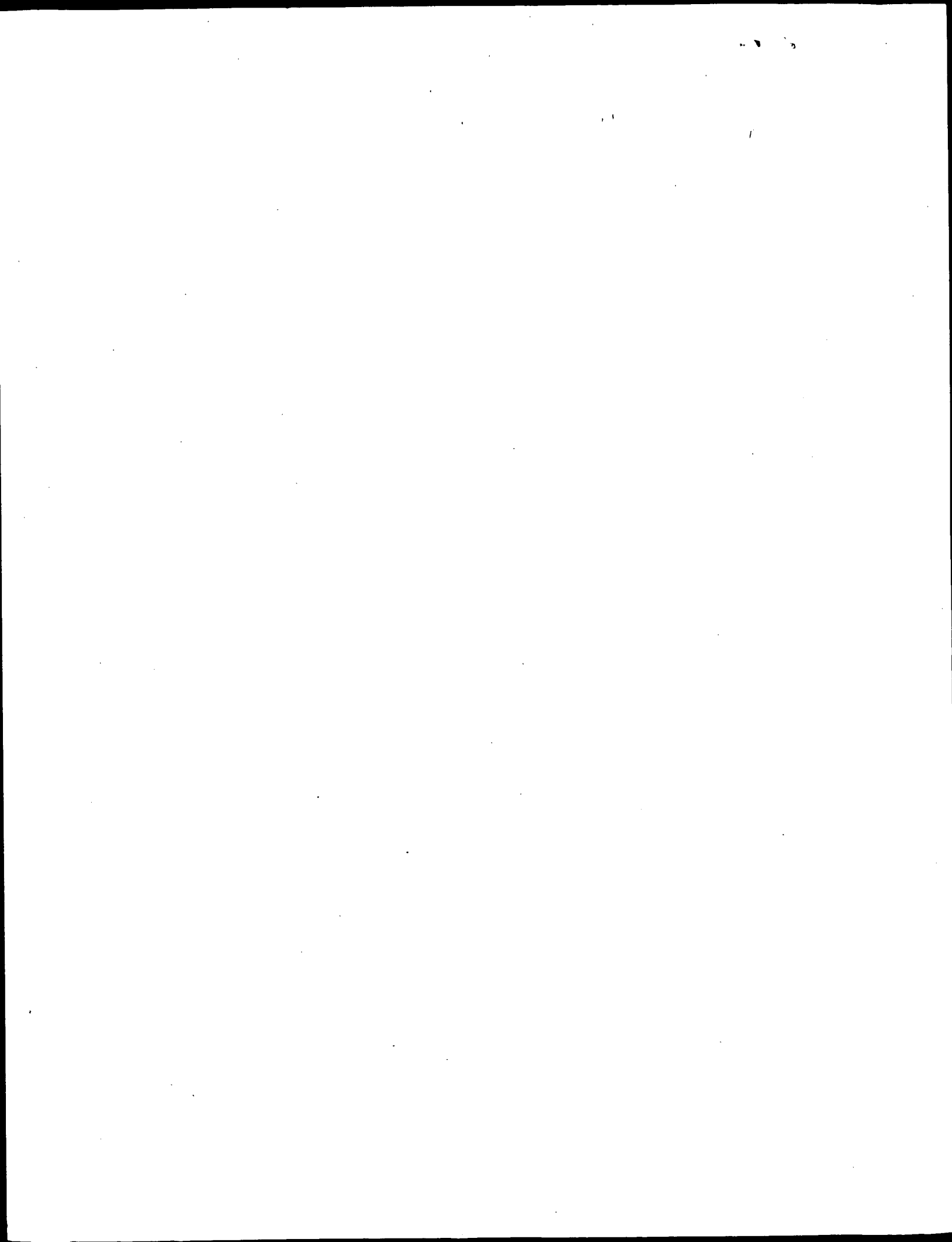
From: Mona Smith
Location: Biotech-Chem Library
CM1-6A01
Phone: 308-3278

mona.smith@uspto.gov

Search Notes

Thank you for using STIC services
Feel free to contact me if you have any questions.

Mona Smith
308-3278



STIC-Biotech/ChemLib

96300

From: Winkler, Ulrike
Sent: Tuesday, June 10, 2003 3:53 PM
To: STIC-Biotech/ChemLib

STIC,
Please search SEQ ID NO 5 of application 09/976605.

Thanks, Ulrike

Ulrike Winkler, Ph.D.
Patent Examiner
Crystal Mall 1, 8D09/ Mail Box 8E12
1911 South Clark Place
Arlington, VA 22202
tel. 703-308-8294
fax. 703-308-4426

RECEIVED
JUN 10 2003
STIC

Searcher: M. Smith
Phone: _____
Location: _____
Date Picked Up: 6/11/03
Date Completed: 6/16/03
Searcher Prep/Review: 3
Clerical: 5
Online time: 5

TYPE OF SEARCH:
NA Sequences: 1
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____



STIC SEARCH RESULTS

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor
308-4258, CM1-1E01

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library CM1 – Circ. Desk



Winkler, Ulrike

From: Winkler, Ulrike
Sent: Tuesday, June 10, 2003 3:53 PM
To: STIC-Biotech/ChemLib

STIC,
Please search SEQ ID NO 5 of application 09/976605.

Thanks, Ulrike

Ulrike Winkler, Ph.D.
Patent Examiner
Crystal Mall 1, 8D09/ Mail Box 8E12
1911 South Clark Place
Arlington, VA 22202
tel. 703-308-8294
fax. 703-308-4426

